

SEQUENCE LISTING

<110> Wright, David A.  
Voytas, Daniel F.

<120> Plant Retroelements and Methods Related Thereto

<130> P-1065A

<140>  
<141>

<150> 60/087125  
<151> 1998-05-29

<150> 09/322478  
<151> 1999-05-28

<160> 165

<170> PatentIn Ver. 2.1

<210> 1  
<211> 18  
<212> DNA  
<213> Glycine max

<400> 1  
tggcgccgtt gccaaattg

18

<210> 2  
<211> 18  
<212> DNA  
<213> Glycine max

<400> 2  
tggcgccgtt gtcggggga

18

<210> 3  
<211> 6  
<212> DNA  
<213> Glycine max

<400> 3  
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6

<210> 4  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 4  
Met Ala Ser Arg Lys Arg Lys  
1 5

<210> 5  
<211> 1263  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 5  
atggcctccc gtaaacgcaa agctgtgccc acacccgggg aagcgccaa ctggactct 60  
tcacgttca ctttcgagat tgcttggcac agataccagg atagcattca gctccggAAC 120  
atccttccag agaggaatgt agagcttggc ccagggatgt ttgatgagtt cctgcaggaa 180  
ctccagaggc tcagatggc ccaggttctg acccgacttc cagagaagtg gattgatgtt 240  
gctctggta aggagttta ctccaaccta tatgatccag aggaccacag tccgaagttt 300  
tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac 360  
accccggtca tcttggcaga gggagaggat tatccagcct actctcagta cctcagcact 420  
cctccagacc atgatgccat cctttccgt ctgtgtactc cagggggacg atttgttctg 480  
aatgttgata gtgccccctg gaagctgtc cggaaggatc tgatgacgct cgccgcagaca 540  
tggagtgtgc tctcttattt taaccttgca ctgacttttc acacttctga tattaaatgtt 600  
gacagggccc gactcaatta tggcttggtg atgaagatgg acctggacgt gggcagcctc 660  
atttctcttc agatcagtca gatcgccag tccatcaattt ccaggcttgg gttcccagcg 720  
ttgatcacaactt cactgtgtga gattcagggg gttgtctctg ataccctgat tttttagtca 780  
ctcagtcctg tgatcaacact tgcctacatt aagaagaact gctggAACCC tgccgatcca 840  
tctatcacat ttcaggggac ccggccgcacg cgccaccagag ctgcggcgac ggcacatctgag 900  
gctcccttc catcccagca tccttctcag ccttttccc agagaccacg gcctccactt 960  
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gacagggggg aagagccttc tggagccgct gctactgagg atcctggcgt tgatgaagac 1200  
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tga 1263

<210> 6  
<211> 421  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 6  
Met Ala Ser Arg Lys Arg Lys Ala Val Pro Thr Pro Gly Glu Ala Ser  
1 5 10 15  
  
Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr  
20 25 30  
  
Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu  
35 40 45  
  
Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu  
50 55 60  
  
Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val  
65 70 75 80  
  
Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His  
85 90 95  
  
Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala  
100 105 110  
  
Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly  
115 120 125  
  
Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His  
130 135 140  
  
Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu  
145 150 155 160  
  
Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr  
165 170 175  
  
Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr  
180 185 190  
  
Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly

195	200	205
Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln		
210	215	220
Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala		
225	230	235
240		
Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu		
245	250	255
Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys		
260	265	270
Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg		
275	280	285
Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro		
290	295	300
Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu		
305	310	315
320		
Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser		
325	330	335
Leu Tyr Gln Gly Gln Gln Ile Ile Gln Asn Leu Tyr Arg Leu Ser		
340	345	350
Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg		
355	360	365
Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu		
370	375	380
Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp		
385	390	395
400		
Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu		
405	410	415
Gly Arg Gly Ser Glx		
420		

<210> 7  
<211> 1596  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 7

atgcgaggta gaactgcac tggagacgtt gttcctatta acttagaaat tgaagctacg 60  
tgtcgccgta acaacgctgc aagaagaaga agggagcaag acatagaagg aagttagttac 120  
acctcaccc tccttcctcc aaattatgct cagatggacg gggAACCGC acaaagagtc 180  
acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg 240  
gaagtccaag cagatctcct tactcaaggg aacctttcc atggcttcc aaatgaagat 300  
ccatatgcgc atctagcctc atacatacag atatgcagca ccgtaaaat cgccggagtt 360  
ccaaaagatg cgatactcct taacctctt tcctttccc tagcaggaga ggcaaaaaga 420  
tggttgcaact cctttaaagg caatagctt agaacatggg aagaagtatg gaaaaattc 480  
ttaaagaagt atttcccaga gtcaaagacc gtcaacgaa agatggagat ttcttatttc 540  
catcaatttc tggatgaatc ccttagcga gcactagacc atttccacgg attgctaaga 600  
aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660  
caactcttaa tcgaaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720  
atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat 780  
gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac 840  
aagctgttga cgagggcagat agaaggccctc atcgaaaccc tcagcaagct gcctcaacaa 900  
ttacaagcga taagttcttccactctt gtttgcagg tagaagaatg ccccacatgc 960  
agagggacac atgagcctgg acaatgtcga agccaacaag acccctctcg tgaagtaaat 1020  
tatataaggca tactaaatcg ttacggattt cagggctaca accagggaaa tccatctgga 1080  
ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggttaatca aggaagaaac 1140  
ttcatgcaag gctcaagttg gacgataaaa ggaatcaat ataaggagca aaggaaccaa 1200  
ccaccatacc agccaccata ccagcaccc agccaaggc cgaatcagca agaaaagccc 1260  
acccaaatag aggaactgct gctcaattc atcaaggaga caagatcaca tcaaaagagc 1320  
acggatgcag ccattcggaa tctagaagtt caaatgggcc aactggcgca tgacaaagcc 1380  
gaacggccca ctagaacttt cggtgctaac atggagagaa gaaccccaag gaaggataaa 1440  
gcagttactga cttagagggca gagaagagcg caggaggagg gtaaggttga aggagaagac 1500  
tggccagaag aaggaaggac agagaagaca gaagaagaag agaaggtggc agaagaaccc 1560  
aagcgtacca agagccagag agcaaggaa gccaaag 1596

<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 8

Met Arg Gly Arg Thr Ala Ser Gly Asp Val Val Pro Ile Asn Leu Glu

1

5

10

15

Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu  
20 25 30

Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn  
35 40 45

Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp  
50 55 60

Phe Ser Asn Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro  
65 70 75 80

Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu  
85 90 95

Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys  
100 105 110

Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn  
115 120 125

Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser  
130 135 140

Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe  
145 150 155 160

Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu  
165 170 175

Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu  
180 185 190

Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser  
195 200 205

Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile  
210 215 220

Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala  
225 230 235 240

Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His  
245 250 255

Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr  
260 265 270

Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu  
275 280 285

Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile  
290 295 300

Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys  
305 310 315 320

Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser  
325 330 335

Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly  
340 345 350

Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe  
355 360 365

Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly  
370 375 380

Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln  
385 390 395 400

Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln  
405 410 415

Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys  
420 425 430

Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu  
435 440 445

Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr  
450 455 460

Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys  
465 470 475 480

Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val  
485 490 495

Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu  
500 505 510

Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala  
515 520 525

Arg Glu Ala Lys

530

<210> 9  
<211> 603  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 9  
tgtgataaat gccagagaac agggggata tctcgaagaa atgagatgcc tttgcagaat 60  
atcatggaag tagagatctt tgactgttg ggcataact tcataggcc ttttcattcg 120  
tcatacgga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaaagcc 180  
atagccacgc caaaggacga tgccaggta gtatcaaattt ttctgaagaa gaacattttt 240  
tcccgtttt gagtcccacg agcattgatt agtataggg gaacgcactt ctgcaacaat 300  
cagttgaaga aagtccctgga gcactataat gtccgacata aggtggccac accttatcac 360  
cctcagacaa atggccaagc agaaatttct aacaggagc tcaagcgaat cctggaaaag 420  
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgtct ctggccatat 480  
aggacagcgt tcaagactcc catcggctta tcaccatttc agctatgtta tggaaaggca 540  
tgtcatttac cagtggagct ggagtacaaa gcatattggg ctctcaagtt gctcaacttt 600  
gac 603

<210> 10  
<211> 201  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 10  
Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met  
1 5 10 15

Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile  
20 25 30

Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu  
35 40 45

Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro

50

55

60

Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe  
65 70 75 80

Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His  
85 90 95

Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg  
100 105 110

His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu  
115 120 125

Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser  
130 135 140

Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr  
145 150 155 160

Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val  
165 170 175

Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr  
180 185 190

Trp Ala Leu Lys Leu Leu Asn Phe Asp  
195 200

<210> 11

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 11

ttggaggctg ggctcatata ccccatctct gacagcgctt gggtaagccc agtacaggtg 60  
gttcccaaga aagggtggaaat gacagtggta cgagatgaga ggaatgactt gataccaaca 120  
cgaactgtca ctgggtggcg aatgtgtatc gactatcgca agctgaatga agcccacacgg 180  
aaggaccatt tccccttacc tttcatggat cagatgctgg agagacttgc agggcaggca 240  
tactactgtt tcttgatgg atactcgaaa tacaaccaga tcgcggtaga ccccagagat 300  
caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360  
gggttatgta atgcaccaggc cacatttcag aggtgcattgc tggccatttt ttcagacatg 420  
gtggagaaaa gcatcgaggt atttatggac gacttctcggtttttggacc ctcatttgac 480

agctgtttga ggaacctaga gagggtaactt cagaggtgcg aagagactaa cttggtaactg 540  
aattgggaaa agtgtcattt catggttcga gagggcatag tccttaggccca caagatctca 600

<210> 12  
<211> 200  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 12  
Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser Ala Trp Val Ser  
1 5 10 15  
  
Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp  
20 25 30  
  
Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met  
35 40 45  
  
Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe  
50 55 60  
  
Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu Ala Gly Gln Ala  
65 70 75 80  
  
Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ala Val  
85 90 95  
  
Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys Pro Phe Gly Val  
100 105 110  
  
Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr  
115 120 125  
  
Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met Val Glu Lys Ser  
130 135 140  
  
Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly Pro Ser Phe Asp  
145 150 155 160  
  
Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg Cys Glu Glu Thr  
165 170 175  
  
Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Arg Glu Gly

180

185

190

Ile Val Leu Gly His Lys Ile Ser  
195                   200

<210> 13

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 13

aaggaagaac cactagccct tccacaggat ctccccatatac ctatggcacc caccaagaag 60  
aacaaggagc gttactttgc acgtttcttg gaaatattca aagggttaga aatcactatg 120  
ccattcgaaaa aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc 180  
accaagaagg ggaagtatat tgacaacgag aatattgtgg taggaggcaa ttgcagtgcg 240  
ataatacataaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccggtgc 300  
accattggaa aggaagccgt aaacaaggcc ctcattgtatc taggagcaag tatcaatctg 360  
atgcccttgtt caatgtgcaa aagaattggg aatttgaaga tagatcccac caagatgacg 420  
cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaaga tggcctggtc 480  
aaggtacgcc acttcacttt tccgggtggac tttgttatca tggatatcga agaagacact 540  
gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600  
gggaaaaggaa acttagagtt gactattgtt aatcagaaga tcaccttga ctttatcaag 660  
gcaatgaagt acccacagga ggggttggaaag tgcttcagaa tagaggagat tggatggaa 720  
gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggt aaatcattta 780  
gactgtctaa ccagtgaaga ggaagaagat ctgaaggctt gcttggaaaa cttggatcaa 840  
gaagacagta ttcctgag   858

<210> 14

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 14

Lys Glu Glu Pro Leu Ala Leu Pro Gln Asp Leu Pro Tyr Pro Met Ala  
1                   5                   10                   15

Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile  
20                   25                   30

Phe	Lys	Gly	Leu	Glu	Ile	Thr	Met	Pro	Phe	Gly	Glu	Ala	Leu	Gln	Gln
35														45	
Met	Pro	Leu	Tyr	Ser	Lys	Phe	Met	Lys	Asp	Ile	Leu	Thr	Lys	Lys	Gly
50														60	
Lys	Tyr	Ile	Asp	Asn	Glu	Asn	Ile	Val	Val	Gly	Gly	Asn	Cys	Ser	Ala
65														80	
Ile	Ile	Gln	Arg	Ile	Leu	Pro	Lys	Lys	Phe	Lys	Asp	Pro	Gly	Ser	Val
85														95	
Thr	Ile	Pro	Cys	Thr	Ile	Gly	Lys	Glu	Ala	Val	Asn	Lys	Ala	Leu	Ile
100														110	
Asp	Leu	Gly	Ala	Ser	Ile	Asn	Leu	Met	Pro	Leu	Ser	Met	Cys	Lys	Arg
115														125	
Ile	Gly	Asn	Leu	Lys	Ile	Asp	Pro	Thr	Lys	Met	Thr	Leu	Gln	Leu	Ala
130														140	
Asp	Arg	Ser	Ile	Thr	Arg	Pro	Tyr	Gly	Val	Val	Glu	Asp	Val	Leu	Val
145														160	
Lys	Val	Arg	His	Phe	Thr	Phe	Pro	Val	Asp	Phe	Val	Ile	Met	Asp	Ile
165														175	
Glu	Glu	Asp	Thr	Glu	Ile	Pro	Leu	Ile	Leu	Gly	Arg	Pro	Phe	Met	Leu
180														190	
Thr	Ala	Asn	Cys	Val	Val	Asp	Met	Gly	Lys	Gly	Asn	Leu	Glu	Leu	Thr
195														205	
Ile	Asp	Asn	Gln	Lys	Ile	Thr	Phe	Asp	Leu	Ile	Lys	Ala	Met	Lys	Tyr
210														220	
Pro	Gln	Glu	Gly	Trp	Lys	Cys	Phe	Arg	Ile	Glu	Glu	Ile	Asp	Glu	Glu
225														240	
Asp	Val	Ser	Phe	Leu	Glu	Thr	Pro	Lys	Thr	Ser	Leu	Glu	Lys	Ala	Met
245														255	
Val	Asn	His	Leu	Asp	Cys	Leu	Thr	Ser	Glu	Glu	Glu	Asp	Leu	Lys	
260														270	
Ala	Cys	Leu	Glu	Asn	Leu	Asp	Gln	Glu	Asp	Ser	Ile	Pro	Glu		
275														285	

<210> 15  
<211> 192  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 15  
tttgaactaa tgtgtgatgc cagtgattat gcagtaggag cagtttggg acagaggaaa 60  
gacaaggat ttcacgccc ctattatgct agcaagggtcc tgaatgaagc acagttgaat 120  
tatgcaacca cagaaaagga gatgcttagcc attgtcttg ccttggagaa gttcaggta 180  
tacttgatag gg 192

<210> 16  
<211> 64  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 16  
Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Val Gly Ala Val Leu  
1 5 10 15

Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys  
20 25 30

Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met  
35 40 45

Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly  
50 55 60

<210> 17  
<211> 12286  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 17

tgataactgc taaaataattg tgaattaata gtagaaaaatt agtcaaattt tggcttaaaa 60  
ttaatttattt agcagttatt tgtgattaaa agtttagaaaa gcaattaagt tgaatttttg 120  
gccatagata tgaaaactga aggtacaaca agcaaaaaggc agcagaaaagt gaagaaaaag 180  
aataaaatct gaagcagacc cagcccaaca cgcgccctta gcgcgcgtca cgcgctaagc 240  
ttgcaaggca gcacaggcac taagcgaggc gttaagcacf aagatgcagg attcggtacg 300  
tgcgctaagc gcgaggcaca cgctaagcgc gcgatccaac agaagcacac gctaagcctg 360  
cagcatgcgc taagcgcgc tacgaaggcc caaagcccatt ttctacaccc ataaatagag 420  
atccaagcca agggagaatg tacaccctgc ctcagagcac ttctctcagc attccaagct 480  
tgagctctcc ctttctctc tatattctt gcttttattt tccattctt ct当地cacc 540  
agttgtaaag cccctcaatg gccatgagtg gttaatcccc tagtacggc ctggtaggcc 600  
taaaaagcca atgatgtatg gtgtacttca agagttatca atgcaaagag gattcattcc 660  
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35 40 45

Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp  
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Phe Ser Asn Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro  
65 70 75 80

Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu  
85 90 95

Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys  
100 105 110

Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn  
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130 135 140

Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe  
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Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu  
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Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu  
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Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser  
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Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His  
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Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr  
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Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu  
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Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile  
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 <213> *Arabidopsis thaliana*

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<212> DNA  
<213> Pisum sativum

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ttggaaaagc gaaagatTTT gccggaaaag agatttataa tcaaccctga aggcacgaac 180  
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<210> 26  
<211> 564  
<212> DNA  
<213> Arabidopsis thaliana

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tcatacggta ataaatatat actggtcgcc gtagactacg tatcaaagtg ggtcgaagct 180  
attgctagtc ctaccaacga tgcaaaagtt gtgctgaagt tggtcaaaac cataatcttc 240  
ccaagatttg gagtcccag ggttagtaatc agtggatggcg gaaagcattt catcaacaag 300  
gttttggaga acctcttggaa gaagcatggg gttaaaggcagg ttgagatctc caatagggag 360  
ataaaaaacaa ttctggaaaaa gactgttggg attacaagga aagactggtc tgcaaagcta 420  
gatgatgcat tatgggctta caggacagct ttcaagaccc ccataggtac aactcccttc 480  
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gcggtaaaac ttctgaactt tgac 564

<210> 27  
<211> 180  
<212> DNA  
<213> Arabidopsis thaliana

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aattggaaaa agtgcattt catggtaag gaaggcatag tattggacca caagatatca 180

<210> 28  
<211> 192  
<212> DNA  
<213> Arabidopsis thaliana

<400> 28  
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gacaagaagc ttcatgtcat atattacgcc agccgaacgt tggatgacgc tcagggaa 120  
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192

<210> 29  
<211> 597  
<212> DNA  
<213> Pisum sativum

<400> 29  
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aaagttgcaa cgggggtggag aatgtgtatt gaatataggc gggtgaatac cgcaactcga 180  
aaggaccatt ttccactccc gttcatggat caaatgctgg aaagactctc cgggcaacaa 240  
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<210> 30  
<211> 192  
<212> DNA  
<213> Pisum sativum

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tatgccacca ctgaaaaaga attacttgcg atagtgtatg cacttgaaaa gtttaggtct 180  
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<210> 31  
<211> 581  
<212> DNA  
<213> Pisum sativum

<400> 31  
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cgaaaaacggt aataattttt ttgaagaaaa acatatttc ccgttgcga accccccgag 240  
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agtggtcaca aaaattggat gaagcggtat gggcataccg taccgcctt aaagctccaa 480  
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581

<210> 32  
<211> 1362  
<212> DNA  
<213> Glycine max

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<210> 33  
<211> 192  
<212> DNA  
<213> Glycine max

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tatgctacca cagaaaaaga aatgttgca attgtttatg cacttgaaaa gttcaaattct 180  
tatttggtag gc 192

<210> 34  
<211> 597

<212> DNA

<213> Glycine max

<400> 34

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<210> 35

<211> 603

<212> DNA

<213> Glycine max

<400> 35

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gac 603

<210> 36

<211> 150

<212> DNA

<213> Glycine max

<400> 36

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tagatcaagt tcttttcaa ttttctttt 150

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<211> 11

<212> DNA  
<213> Glycine max

<400> 37  
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<210> 38  
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15

<210> 39  
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<212> DNA  
<213> Glycine max

<400> 39  
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27

<210> 40  
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<212> DNA  
<213> Glycine max

<400> 40  
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9

<210> 41  
<211> 16  
<212> DNA  
<213> Glycine max

<400> 41  
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16

<210> 42  
<211> 775  
<212> DNA  
<213> Nicotiana tabacum

<400> 42

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<210> 43

<211> 259

<212> PRT

<213> Nicotiana tabacum

<400> 43

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Gly Val Ile Tyr Pro Ile Tyr Asp Ser Ser Glx Thr Ser Pro Val Gln  
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Cys Val Pro Lys Lys Gly Gly Met Thr Val Val Thr Asn Glu Lys Asn  
35 40 45

Glu Leu Ile Pro Thr Arg Met Val Thr Gly Trp Arg Val Cys Met Asp  
50 55 60

Tyr Arg Lys Leu Asn Lys Leu Thr Arg Lys Asp His Phe Pro Phe Pro  
65 70 75 80

Phe Leu Asp Gln Met Leu Asp Arg Leu Ala Cys Arg Ala Phe Tyr Cys  
85 90 95

Phe Leu Asp Val Glx Ser Gly Tyr Ser Gln Ile Phe Ile Ala Pro Glx  
100 105 110

Asp His Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Tyr  
115 120 125

Lys Arg Met Pro Phe Gly Leu Cys Asn Ala Leu Ala Asn Phe Tyr Arg  
130 135 140

Cys Met Met Ala Ile Phe Thr Asp Met Val Lys Asp Tyr Leu Lys Val  
 145 150 155 160  
  
 Phe Met Asp Asp Phe Ser Met Val Gly Asp Ser Phe Asp Asp Cys Leu  
 165 170 175  
  
 Glu Asn Leu Asp Lys Val Leu Ala Arg Tyr Glu Glu Thr Asn Leu Val  
 180 185 190  
  
 Leu Asn Trp Glu Lys Cys His Phe Met Ile Glu Glu Gly Ile Val Leu  
 195 200 205  
  
 Gly His Lys Ile Ser Asn Asn Gly Ile Glu Val Asp Lys Ala Lys Ile  
 210 215 220  
  
 Lys Val Ile Ser Lys Leu Thr Pro Pro Thr Leu Val Lys Gly Val Arg  
 225 230 235 240  
  
 Ser Phe Leu Gly His Ala Gly Phe Tyr Gln Phe Phe Ile Lys Asp Phe  
 245 250 255  
  
 Thr Lys Val

<210> 44  
 <211> 761  
 <212> DNA  
 <213> Nicotiana tabacum

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<210> 45

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 45

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20 25 30

Val Gly Met Thr Val Val Lys Asn Ser Lys Asn Glu Leu Ile Pro Thr  
35 40 45

Arg Thr Ile Thr Gly Trp Arg Val Cys Met Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Val Thr Cys Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met  
65 70 75 80

Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Glu Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Leu Ile Ala Pro Glu Asp Pro Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Phe Val Phe Ser Arg Met Pro Phe  
115 120 125

Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
130 135 140

Phe Ser Tyr Met Val Lys Asp Ile Phe Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Val Gly His Ser Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg  
165 170 175

Val Leu Ala His Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Glu Glu Gly Ile Asn Leu Trp His Lys Ile Ser  
195 200 205

Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg  
210 215 220

Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Cys Phe Leu Gly His

225

230

235

240

Ala Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Ser Lys Val

245

250

<210> 46

<211> 762

<212> DNA

<213> Nicotiana tabacum

<400> 46

gtgcgttaagg aggtgtttaa gttgttggat gttggggttg tgtaccccat ctctgatagc 60  
tcctgcattt cgccggtgca atgtgtaccg aagaagggtg gcatgaccgt gttgcaaata 120  
tcgcaaaatg ggttattcc taccaggatc gtcaccgggt ggaaggatg catggattac 180  
cgaaaagttga ataaaagtgc acgcaggat cactttccat tgcctttct tgatcagatg 240  
ttagatcgac ttgctggcg tgccttctac tttttcttgg atgggtattc tggatacaac 300  
caaatacttca ttactccgga agatcaggag aagacaacat tcacttgtcc atatggcacc 360  
tttgctttt ctaggatgcc ttttgggttg tgtaatgcac cgactacatt ctagcggtat 420  
atgatggcca ttttcaactga tatggtgaa gatattttgg aggtgttcat ggacgacttt 480  
agtgttgggt gtgattcatt tgatgaatgt ttgaataatc ttgatagagt gttggcccat 540  
tgtaaagaaaa ccaatcttgc tcttaattgg gagaatgcc acttcatggc tgaggaggc 600  
atagttcttg ggcataaaaat tttaaagcat ggtatagagg tggacaaagc aaaaattgtat 660  
gtgatttcaa ggctccctcc ccctacttct gtcaagggag tgagaagttt tcttaggcat 720  
gcggggttct accggagatt catcaaagat ttcaccaaag tt 762

<210> 47

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 47

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Val Val Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Ser Cys Ile Ser Pro Val Gln Cys Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Ala Asn Ser Gln Asn Gly Leu Ile Pro Thr  
35 40 45

Arg Ile Val Thr Gly Trp Lys Val Cys Met Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met  
65 70 75 80

<210> 48  
<211> 760  
<212> DNA  
<213> Nicotiana tabacum

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<400> 48
gcggaaggag gtcgtcaagc tgttggatgt cggtgttgt taccccatat ttgatagctc 60
ttggactttg ccggtgcaat atgtgccgaa gaagggttgt atgaccgtgg ttaccaatgt 120
aaaaaatgag ttgattccta ccaggactgt caccgggtgg agggtgtgca tggattacca 180
caaattgaat aaagtgaccc gcaaggatca ctccattt cctttctt atcagatgtt 240
agacagactt gctgggtgtg cttctactg ttcttgat gggtattctg ggtgcaacaa 300
aattttgatt gcacaaaag atcaggagaa gaccacctt acttgtacgt atggtaacctt 360
tgtctttct agatgtcat ttgggttgtg taatgcaccc actacattct agaggtgtat 420
gatggccata ttacactaca tggtgaggaa catttggag gtgttatgg atgacttcag 480
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tgttgggt gactagttg atgaatgtt gaaaaatctt gatagagtgt tggcccggtt 540  
tgaagaagcc aaccctgtgc ttaattggga gaaatgccac ttcatgggtt aggagggcat 600  
agtcccttagc cataaaattt caaagcatgg tatagaggtg gacaaagcaa aaattgaagt 660  
gatttcaagg ctccttcccc ctacttctgt caagggagtt agaagtttc ttgggcattc 720  
ggggttctac tggagattca tcaaagactt cacgaagggtt 760

<210> 49

<211> 253

<212> PRT

<213> Nicotiana tabacum

<400> 49

Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro Ile  
1 5 10 15

Phe Asp Ser Ser Trp Thr Leu Pro Val Gln Tyr Val Pro Lys Lys Gly  
20 25 30

Gly Met Thr Val Val Thr Asn Val Lys Asn Glu Leu Ile Pro Thr Arg  
35 40 45

Thr Val Thr Gly Trp Arg Val Cys Met Asp Tyr His Lys Leu Asn Lys  
50 55 60

Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met Leu  
65 70 75 80

Asp Arg Leu Ala Gly Cys Ala Phe Tyr Cys Phe Leu Asp Gly Tyr Ser  
85 90 95

Gly Cys Asn Lys Ile Leu Ile Ala Pro Lys Asp Gln Glu Lys Thr Thr  
100 105 110

Phe Thr Cys Thr Tyr Gly Thr Phe Val Phe Ser Arg Met Ser Phe Gly  
115 120 125

Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Cys Met Met Ala Ile Phe  
130 135 140

Thr Tyr Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe Ser  
145 150 155 160

Val Val Gly Asp Glx Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg Val  
165 170 175

Leu Ala Arg Cys Glu Glu Ala Asn Leu Val Leu Asn Trp Glu Lys Cys  
180 185 190

His Phe Met Val Glu Glu Gly Ile Val Leu Ser His Lys Ile Ser Lys  
195 200 205

His Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Ser Arg Leu  
210 215 220

Leu Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Gly His Ala  
225 230 235 240

Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 50

<211> 762

<212> DNA

<213> Oryza sativa

<400> 50

gtgcgttaagg aggtgtttaa gttcctgtat gccaggatta tttatctcgat accatacagc 60  
gagtgggtta gcccagttca ggtcgtgcca aagaaggag gaatgacggc cgttgcataat 120  
gctcaaaatg aactaatccc gcaacgaacc gtaaccggat ggagaatgtg catcgattac 180  
aggaaaactta acaaggctac aaaaaaggat catttcccgcc tacccttcat tgatgaaatg 240  
tttggaaacggc tggcaaatac ttcccttc tggatgttcc atgggtattc aggatatcat 300  
caaattccca tccatccgga ggaccagagt aagactacgt tcacatgtcc atatggcacc 360  
tatgcgtatc gtaggatgcc ctttggactg tgcacactc ctgcacatctt ccaaagggtgt 420  
atgatgtcta ttttctcgga catgatcgag gatatcatgg aagtcttcat ggatgacttc 480  
tcggctatg gaaagacttt gggtcattgt ctgcagaatc tagacaaatgt ctacaacga 540  
tgccaaagaaa aggacctgt gcttaactgg gaaaagtgcc atttcatggt ctgtgaagg 600  
atagttcttg ggcacatcgagt gtccgaacga ggagtcgaag ttgatcgtgc taaaattgtat 660  
gtgatagatc agcttcctcc acccgtgaac atcaaaggaa tccgcagctt cttggtcac 720  
gctggcttt atagaagggtt catcaaggac ttccacaaaag tt 762

<210> 51

<211> 254

<212> PRT

<213> Oryza sativa

<400> 51

Val Arg Lys Glu Val Phe Lys Phe Leu Tyr Ala Arg Ile Ile Tyr Leu  
1 5 10 15

Val Pro Tyr Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Ala Val Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln

35

40

45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Thr Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Lys Thr Leu Gly His Cys Leu Gln Asn Leu Asp Lys  
165 170 175

Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Cys Glu Gly Ile Val Leu Gly His Arg Val Ser  
195 200 205

Glu Arg Gly Val Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln  
210 215 220

Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Phe Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 52

<211> 761

<212> DNA

<213> Oryza sativa

<400> 52

gtgcgcaagg aggtttgaa attgctgcat gccaggatta tctatcccg accatacagt 60  
 gagagggtta gcccagtcca gggttgcgc aagaaggag gaatggcggt cgttgc当地 120  
 gtcagaatg aactaattac gcaacaaacc gtaaccggat ggaggatgtg tatcgattac 180  
 aggaaaactca acaaggctac aaaaaaggat cattccccgc tacccttcat tggtgaaatg 240  
 ttggAACGGC tggcaaatca ttccttctt tggttcccttg atggatattt cgatcatcat 300  
 caaattccca tccatccgga ggactagagt aagactacgt tcacatgtcc atatggcacc 360  
 tatgcgtatc ataggatgtc ctggactg tgcaacgctc ctgc当地ctt ccaagggtgta 420  
 tgatgtctat tttctcgac atgatcgagg atatcatgga agtcttcatg gatgacttct 480  
 cggctatgg aaagacttgc ggtcattgtc tgcaaaatct agacaaaagtc ttacaacgat 540  
 gccaagaaaa ggacctggtg cttaactggg aaaagtgaca tttcatggtc cgtgaaggga 600  
 tagttcttgg gcatcgagtg ttgc当地acaag gaatcgaagt tgatcatgct aaaattgatg 660  
 tgatagatca gcttcctcct cccgtgaaca tcaaaggat cc当地cagctc ttgggtcatg 720  
 tcggctttta tagaaggatc atcaaggact tcactaaagt t 761

<210> 53

<211> 254

<212> PRT

<213> Oryza sativa

<400> 53

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Ala	Arg	Ile	Ile	Tyr	Pro
1				5											

Val	Pro	Tyr	Ser	Glu	Arg	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
20														30	

Gly	Gly	Met	Ala	Val	Val	Ala	Asn	Ala	Gln	Asn	Glu	Leu	Ile	Thr	Gln
35							40							45	

Gln	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
50							55							60	

Lys	Ala	Thr	Lys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Val	Glu	Met
65							70							80	

Leu	Glu	Arg	Leu	Ala	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
85														95	

Phe	Gly	Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Glu	Asp	Glx	Ser	Lys	Thr
100							105							110	

Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	His	Arg	Met	Ser	Phe
115							120							125	

Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
130							135							140	

Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
  
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Gln Asn Leu Asp Lys  
 165 170 175  
  
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
  
 Glx His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Phe  
 195 200 205  
  
 Glu Gln Gly Ile Glu Val Asp His Ala Lys Ile Asp Val Ile Asp Gln  
 210 215 220  
  
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
  
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 54  
 <211> 762  
 <212> DNA  
 <213> Oryza sativa

<400> 54  
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 gagtggttca gcacagtcca gggtggccg aagatggat gaatgacggt cgttgc当地 120  
 gctcaaaaata aacttatccc gcaaccaacc ataaccggat ggaggatgtg catagactac 180  
 aggaaaactca acaaggctac aaaagaggat cattttccgc tacccttcat tgatgaaatg 240  
 ttggAACGGA tgacaaatca ttcccttctc tgttccttg atgggtattc cgatatcat 300  
 caaattccca tccgtccaga ggaccagagt aagactacgt tcacatgtcc atatggcacc 360  
 tatgcgtatc gttagatgtc ctccggactg tgcaacgctc ctgc当地ctt ccaaagggtgt 420  
 atgttgc当地 ttttctcgga catgatcgaa gatatcatga aagtcttcat ggatgacttc 480  
 tcagttatg gaaagacttt cggtcattgt ctgtagaatc tagacaaaatg cttacaacga 540  
 tgccaaagaaa atgaccttagt gtttaatgg gaaaagtgcc attttatggt ccgtgaagg 600  
 atagttcttg ggc当地cgagt atccgaatga ggaatc当地ag ttgatc当地gc当地 taaaatcgat 660  
 gttatagatc aaattc当地tcc tcctgc当地at atcaaaggaa tccgc当地gtt cttgggacat 720  
 gccggcttt atagaaggat cctcaaggac ttccacaaaag tt 762

<210> 55  
 <211> 254  
 <212> PRT  
 <213> Oryza sativa

<400> 55

Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Thr  
1 5 10 15

Val Pro Cys Ser Glu Trp Val Ser Thr Val Gln Val Gly Pro Lys Met  
20 25 30

Gly Glx Met Thr Val Val Ala Asn Ala Gln Asn Lys Leu Ile Pro Gln  
35 40 45

Pro Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Met Thr Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile Arg Pro Glu Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Leu Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Asp Ile Met Lys Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Glx Asn Leu Asp Lys  
165 170 175

Val Leu Gln Arg Cys Gln Glu Asn Asp Leu Val Phe Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Ser  
195 200 205

Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln  
210 215 220

Ile Arg Pro Pro Ala Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Leu Lys Asp Phe Thr Lys Val  
245 250

<210> 56  
<211> 762  
<212> DNA  
<213> Oryza sativa

<400> 56

gtgcgttaagg aggtcttcaa gctcttgcattccgat gcccggat tttatccgt accatataga 60  
gagtgggtta gccccgtcta ggttatgccg aagaagggac gaatgacggt cattgcaaat 120  
gctcaaaatg aacttattcc gcaacgaaca gtaaccggat ggaggatgtg catagattac 180  
atgaaactta acaaggctac gaaaaaggat catttccac tacccttcattt tgatgaaaatg 240  
tttggAACGGC tggccaaatca ttctttcttc cgtttcccttg atgggtattc taggtatgtat 300  
caaattccca tccatccgga ggaccaaagt aagactacgt tcacatgttc gtatgataacc 360  
tatgcttatac gtaggatgtc ctccggactg tgcaacgctc ctgcattttt ccaaagggtgt 420  
atgatgtcta ttttctccga catgattaag gacattatgg aagtcttcattt gcatgacttc 480  
tctatttatg gaaagacctc cggtcattgt ctacaaaatt tagacaaaat tttgcaacga 540  
tgccaagaga aggacctggt acttaatgg gaaaagtgtc atttcatggt ccgtgaaggg 600  
atagttctta gtcatcgagt gtccgaataa ggaatcgaag ttgatcgtgc taaaaactat 660  
gtaatagatt agcttccttc tcctgtgaac attaagggga tccgcaattt tttgggacat 720  
gctggctttt atagaagggtt catcaaagac ttcacaaagg tt 762

<210> 57  
<211> 254  
<212> PRT  
<213> Oryza sativa

<400> 57

Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Glu Ile Ile Tyr Pro  
1 5 10 15

Val Pro Tyr Arg Glu Trp Val Ser Pro Val Glx Val Met Pro Lys Lys  
20 25 30

Gly Arg Met Thr Val Ile Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln  
35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Met Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Arg Phe Leu Asp Gly Tyr  
85 90 95

Ser Arg Tyr Asp Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr

100	105	110
Thr Phe Thr Cys Ser Tyr Asp Thr Tyr Ala Tyr Arg Arg Met Ser Phe		
115	120	125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile		
130	135	140
Phe Ser Asp Met Ile Lys Asp Ile Met Glu Val Phe Met His Asp Phe		
145	150	155
Ser Ile Tyr Gly Lys Thr Ser Gly His Cys Leu Gln Asn Leu Asp Lys		
165	170	175
Ile Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Arg Val Ser		
195	200	205
Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Asn Tyr Val Ile Asp Glx		
210	215	220
Leu Pro Ser Pro Val Asn Ile Lys Gly Ile Arg Asn Phe Leu Gly His		
225	230	235
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 58  
 <211> 762  
 <212> DNA  
 <213> Hordeum vulgare

<400> 58  
 gtgcgcagg aggttagaa gttcctggaa gcaggtatca tctatcggt tgctcatagt 60  
 gattgggtga gtcgggtgca ttgtgtccct aagaagggag gcattaccgt tggcccta 120  
 gataaggatg aattgatccc acagaggact attactggct ataggatggt gattgatttt 180  
 aggaaattga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaa 240  
 cgagaaaggc tgtctaaaca cacacacttc tgcttctaa acggtttattt tggtttctcc 300  
 caaataccag ttgcacaatc tgatcaggag aaaaccactt tcacctgccc ttttggtaca 360  
 tttgcttata gacgtatgac ttttggctt tgtaatgcac ctgcctccctt tcaaagatgt 420  
 atgatggcta tattccctga cttttgtgaa aagattgtt aggttttcat ggatgacttc 480  
 tccatattacg gatttccctt tgatgatgc ctcagcaacc ttgatcgagt cttgcagaga 540  
 tgtaaagaca ccaatctttt cttgaattgg aagaagtgcc actttatggt taatgacggc 600  
 atcgctttag gacataaatt ttctgaaaga ggtattgaag tcgataaggc taaggttgat 660  
 ggaatcgaga aaatgccata cccccacagat atcaaaggga taagaagttt cttgggtcat 720

gctggtttct atagaagggtt cataaaaagac ttcactaagg tt

762

<210> 59

<211> 254

<212> PRT

<213> Hordeum vulgare

<400> 59

Val Arg Lys Glu Val Glx Lys Phe Leu Glu Ala Gly Ile Ile Tyr Arg  
1 5 10 15

Val Ala His Ser Asp Trp Leu Ser Arg Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
35 40 45

Arg Thr Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Arg Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asn Gly Tyr  
85 90 95

Phe Gly Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Thr Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ala Ile  
130 135 140

Phe Pro Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Phe Leu Asn Trp Lys Lys  
180 185 190

Cys His Phe Met Val Asn Asp Gly Ile Val Leu Gly His Lys Phe Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Gly Ile Glu Lys  
210 215 220

Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 60

<211> 762

<212> DNA

<213> Hordeum vulgare

<400> 60

gtgcgttaag aggtcctaaa gttcctggaa gcgggttatta tctatcctgt tgctcacaac 60  
gattgggtga gtccggtgca ttgcgtccct aagaaggat gcattaccgt tgcctcta 120  
gataaggatg aattgatccc acataggatt attactggct ataggatggt gatcgatttt 180  
aggaaaatga ataaagccac taggaaagaa cattaccctt tgccttttag cgaccaaatg 240  
ctagaaaagt tgtctaaaca cacacacttc tgctttctag acggttattc tagttctcc 300  
caaatactag ttgcacaatc tgatcaggag aaaaccactt tcacacctt gttcggtacc 360  
tttgcttata gacgtatgcc ttttggctt tgtaatgcac ctgcccac 420  
atgatggcta tattctctga cttttgtgaa aagtttgc aggtttcat ggatgacttt 480  
tccggttacg gatccctt tgatgattgc ctcaacaacc ttgatcgggt ctgcagaga 540  
tgtaaagata ctaatctgt cttgaattgg gagaagtgcc actttatggt taatgaaggc 600  
atcgtcttag gacataaaat ttccgaaaga ggtattgaat tcgataaggc taaggttgg 660  
gcaatcaaga aaatgccata cccccacagat atcaaaggta taagaagg 720  
gctggtttct atagaagg 762  
tttacaaagg tt

<210> 61

<211> 254

<212> PRT

<213> Hordeum vulgare

<400> 61

Val Arg Lys Glu Val Leu Lys Phe Leu Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Ala His Asn Asp Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
20 25 30

Gly Cys Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro His  
35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Met Asn  
50 55 60

Lys	Ala	Thr	Arg	Lys	Glu	His	Tyr	Pro	Leu	Pro	Phe	Ser	Asp	Gln	Met
65															80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
85															95
Ser	Ser	Phe	Ser	Gln	Ile	Leu	Val	Ala	Gln	Ser	Asp	Gln	Glu	Lys	Thr
100															110
Thr	Phe	Thr	Tyr	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
115															125
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
130															140
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Phe	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145															160
Ser	Val	Tyr	Gly	Ser	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Leu	Asp	Arg
165															175
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
180															190
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
195															205
Glu	Arg	Gly	Ile	Glu	Phe	Asp	Lys	Ala	Lys	Val	Gly	Ala	Ile	Lys	Lys
210															220
Met	Pro	Tyr	Pro	Thr	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Val	His
225															240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
245															

<210> 62  
<211> 757  
<212> DNA  
<213> Hordeum vulgare

<400> 62  
gaaaagagggt tgtgaagctc ctggatgaag gtattatcta tcatgttgct catagcgatt 60  
gggtgagtcc ggtgcatagc gttcctaaga agggaggcat taccgttgtc cctaattgata 120  
aggatgaatt gatcccgcag aggattatca ctggctatag gatggtgatc gatttcagga 180  
aactgaataa agccactagg aaagatcatt accctttgcc ttttatcgac catatgctag 240

aaagggttgc caaactcaca cacttctgct ttcttagacgg ttattctagt ttctccaaa 300  
taccagggtgc acaatctgat caggagaaaa ccacccac ctgcccttc ggtacccccc 360  
cttatagacg tatgccttt ggcttatgta atgcacctgc caccccaa agatgtatga 420  
tggctatatt ctctaacttt tgtgaaaata ttgtcgaggt tttcatggat gactttccg 480  
tttacgggtc ttctttgtat gattgcctca gcaacccctga tcgagttca cagagatgt 540  
aagacaccaa tcttgtcttg aatggggaga agtgcaccc tattggtaat gaaggcatcg 600  
tcttaggaca taaaattct gaaagaggtt ttgaagtcga taaggctaag gtgtatgcaa 660  
tcgacaaaat gccatcccc acagatatca aaggtataag aagttccctt ggtcatggtg 720  
gtttctatag aaggtttatac aaagattca caaaggt 757

<210> 63  
<211> 251  
<212> PRT  
<213> *Hordeum vulgare*

<400> 63  
Lys Glu Val Val Lys Leu Leu Asp Glu Gly Ile Ile Tyr His Val Ala  
1 5 10 15  
  
His Ser Asp Trp Val Ser Pro Val His Ser Val Pro Lys Lys Gly Gly  
20 25 30  
  
Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln Arg Ile  
35 40 45  
  
Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn Lys Ala  
50 55 60  
  
Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp His Met Leu Glu  
65 70 75 80  
  
Arg Leu Ser Lys Leu Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser  
85 90 95  
  
Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr Thr Phe  
100 105 110  
  
Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu  
115 120 125  
  
Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile Phe Ser  
130 135 140  
  
Asn Phe Cys Glu Asn Ile Val Glu Val Phe Met Asp Asp Phe Ser Val  
145 150 155 160  
  
Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg Val Leu

165

170

175

Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Gly Glu Lys Cys His  
180 185 190

Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser Glu Arg  
195 200 205

Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Asp Lys Met Pro  
210 215 220

Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His Gly Gly  
225 230 235 240

Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys  
245 250

<210> 64

<211> 740

<212> DNA

<213> Hordeum vulgare

<400> 64

gtgcgtaaag aggtgattaa attcctagaa gaaggtatta tctatcctgt tgctcacagc 60  
gattgggtga gtccggtgca ttgcattcct aagaaaggag gcattaccgt tgtcccta 120  
gataaggatg aattgatccc atagaggatt attactggct ataggatggt gattgatttt 180  
aggaagttaa ataaagccac taggaaagat cattaccctt tgccttttat cgaccaa 240  
ctagaaaggc tgtctaaaca cacacacttc ttgtttctgg acggttatac tggttctcc 300  
caaataccag ttgcacaatt tgatcaggag aaaaccactt taacctgaca tttcggtacc 360  
tttgcttata tacgtatgcc ttttggctt tgtaatgcac ctgccacctt tcaaagatgt 420  
atgatggcta tattctccga cttctgtgaa aagattgtca atgtttcat ggataacttc 480  
tccgtttacg ggtgttccctt tgatgatgc ctcaacaacg ttgatcgagt cttacagaga 540  
tgtaaggaca ccaatgttgt cttgaattgg gagaagtgtc actttatggtaatgaaggc 600  
atcgctttag gacataagat ttctgaaaaga ggtattaaag ttgataaggc taagggtt 660  
gcaatcgaga aaatgccata tccacagata tcaaaggat aagaagttt cttggcata 720  
ctggtttcta tagaagg 740

<210> 65

<211> 247

<212> PRT

<213> Hordeum vulgare

<400> 65

Val Arg Lys Glu Val Ile Lys Phe Leu Glu Glu Gly Ile Ile Tyr Pro  
1 5 10 15

Val	Ala	His	Ser	Asp	Trp	Val	Ser	Pro	Val	His	Cys	Ile	Pro	Lys	Lys
					20			25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Glx
					35			40					45		
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn
					50			55				60			
Lys	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
					65			70			75		80		
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Leu	Phe	Leu	Asp	Gly	Tyr
					85				90				95		
Thr	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ala	Gln	Phe	Asp	Gln	Glu	Lys	Thr
					100				105				110		
Thr	Leu	Thr	Glx	His	Phe	Gly	Thr	Phe	Ala	Tyr	Ile	Arg	Met	Pro	Phe
					115			120			125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
					130			135			140				
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Val	Asn	Val	Phe	Met	Asp	Asn	Phe
					145			150			155		160		
Ser	Val	Tyr	Gly	Cys	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Val	Asp	Arg
					165				170			175			
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Val	Val	Leu	Asn	Trp	Glu	Lys
					180				185			190			
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
					195			200			205				
Glu	Arg	Gly	Ile	Lys	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Glu	Lys
					210			215			220				
Met	Pro	Tyr	Pro	Thr	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
					225			230			235		240		
Ala	Gly	Phe	Tyr	Arg	Arg	Phe									
					245										

<210> 66

<211> 762

<212> DNA

<213> Avena sativa

<400> 66

gtgcgaaagg aggtttcaa gctcatggat gctggatttta tttaccctat tgctgatagt 60  
gaatgggtta gtcatgttca ttgtgttccct aaaaagggag gtattaccgt tgtcccta 120  
gataatgatg agcttattcc tcaaagaata gtggtaggct ataggatgtg catcgatttt 180  
aggaaaagtca ataaaagttac taagaaaat cactacccgc ttccctttat tgcataatg 240  
ttggaaaat tttctaaaaa gaccatttt tggttcttg atggtttattc tggttctct 300  
caaattgttgc taaaacaaca agatcaagaa aaaactactt ttacttgccc ttatgaaact 360  
tatgcttata gatgtatgcc ttgtgttta tgtaatgctc ctctacttt cctaagggtgc 420  
atgtctgcata tccttcattgg ttgtgtgag gaaattgttag aagtgttcat ggacgacttt 480  
tctgtctacg gaacctcttt tgataattgt ctgcacaacc ttgataaagt ttacagaga 540  
tgtgaaggaa ctaatcttgc tcttaattgg gagaaatgcc acttcatggta taatgaaggg 600  
attgttcttg ggcataaagt ttctaaaaga ggcatagaag ttgatagagc taagggttag 660  
gcaattgaga agatgccatg tccaagagac atcaaaggta ttctgtat ccttggtcat 720  
gctggtttct ataggaggaa catcaaagac ttccacaaagg tt 762

<210> 67

<211> 254

<212> PRT

<213> Avena sativa

<400> 67

Val Arg Lys Glu Val Phe Lys Leu Met Asp Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Ile Ala Asp Ser Glu Trp Val Ser His Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln  
35 40 45

Arg Ile Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn  
50 55 60

Lys Val Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Phe Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Phe Ser Gln Ile Val Val Lys Gln Gln Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Cys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ser Thr Phe Leu Arg Cys Met Ser Ala Ile  
130 135 140

Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys  
165 170 175

Val Leu Gln Arg Cys Glu Gly Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Lys Arg Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys  
210 215 220

Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 68  
<211> 762  
<212> DNA  
<213> Avena sativa

<400> 68  
gtgcgcaaag aggtctttaa gttccttgat gctggtatta tttaccctat tgctgatagt 60  
caatgggtta gccttgttca ttgtgtcccc aagaaagggg gaataactgt tgtgcctaatt 120  
gaagataatg agcttataacc ccaaagagta gtgggtgtgt atagaatgtg cattgatttt 180  
agaaggatta ataaaagttaggaaagat cattatcctt tgccctttat tgatcaaatg 240  
cttgagaggt tgtccaaaaa gactcacttt tgtttcttg atggtcattc tgggtttct 300  
caaattgttg tgaaagcaca agaccaagag aaaactactt tcacttgtcc ttatggtaact 360  
tatgattata ggcgtatgcc ttttggttta tgtaatgctc ctgctacctt tcagagatgt 420  
atgtctgcta tatttcatgg ttttggtaa gaaattgtgg aggtttcat ggacgatttt 480  
tctgtctatg gaacttcttt tgataactgt ttgcacaacc ttgataaaatt ttgcagaga 540  
tttgaagaaa ccaacccctgt tcttaattgg gagaaatgcc atttcatggta taatgaaggg 600  
attgttcttg gacacaaagat ctcagaaaga ggcattgaag ttgacagagc caaaattgaa 660  
gcaattgaga acatgccttg cccttagagat attaaaggta ttcgtagtat ccttggcat 720  
gctggttct atagtaggtt catcaaagac tttacaaaag tt 762

<210> 69

<211> 254

<212> PRT

<213> Avena sativa

<400> 69

Val Arg Lys Glu Val Phe Lys Phe Leu Asp Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Ile Ala Asp Ser Gln Trp Val Ser Leu Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Glu Asp Asn Glu Leu Ile Pro Gln  
35 40 45

Arg Val Val Val Val Tyr Arg Met Cys Ile Asp Phe Arg Arg Ile Asn  
50 55 60

Lys Val Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly His  
85 90 95

Ser Gly Phe Ser Gln Ile Val Val Lys Ala Gln Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Asp Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile  
130 135 140

Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys  
165 170 175

Phe Leu Gln Arg Phe Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Ala Ile Glu Asn  
210 215 220

Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His

225

230

235

240

Ala Gly Phe Tyr Ser Arg Phe Ile Lys Asp Phe Thr Lys Val

245

250

<210> 70

<211> 756

<212> DNA

<213> Avena sativa

<400> 70

aaggaggtt ttaaactcct ttagtgttgg attatattacc ctattgctga tagtgaatgg 60  
gttagtcttg ttcatgtgt tcctaaaaag ggaggtatta ccgttgttcc taatgataat 120  
gatgagctt ttcctcaaag aatagtggta ggctatagga tgcgtataga ttttaggaaa 180  
gttaataaaag ttactaagaa agatcaactac ccgccttcctt ttattgatca aatgttgaa 240  
aggttgtcta aaaagaccca ttttgtttt cttgtatggtt actctagctt ctctcaaatt 300  
gctgttaaac aacaagatca agaaaaact actttactt gcccattatgg aacttttgct 360  
tatagacgta tgcctattgg tttatgtaat gctcctgcta ctttcaaag gtgtatgtct 420  
gctatatttc atgggttttg tgagggaaatt gtagaagtgt tcatggatga cttttctgtc 480  
tatggaaactt ctttgataa ttgcctgcac aaccttgata aagtttgca gagatgtgaa 540  
gaaactaata ttgttcttaa ttgggagaaa ttccacttca tggtaatga agggattgtc 600  
cttgggcata aagttctaa aagaggcata gaagttgata gagctaaggt tgaggcaatt 660  
gagaagatgc catgcccaag agacatcaaa ggtatacgta gtatccttgg tcatgctgg 720  
ttctatagaa ggtttatcaa agacttcaca aaggtt 756

<210> 71

<211> 252

<212> PRT

<213> Avena sativa

<400> 71

Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro Ile Ala  
1 5 10 15

Asp Ser Glu Trp Val Ser Leu Val His Cys Val Pro Lys Lys Gly Gly  
20 25 30

Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln Arg Ile  
35 40 45

Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn Lys Val  
50 55 60

Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met Leu Glu  
65 70 75 80

Arg	Leu	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Ser
					85					90					95
Phe Ser Gln Ile Ala Val Lys Gln Gln Asp Gln Glu Lys Thr Thr Phe															
					100					105					110
Thr Cys Pro Tyr Gly Thr Phe Ala Tyr Arg Arg Met Pro Ile Gly Leu															
					115					120					125
Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile Phe His															
					130					135					140
Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe Ser Val															
					145					150					160
Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys Val Leu															
					165					170					175
Gln Arg Cys Glu Glu Thr Asn Ile Val Leu Asn Trp Glu Lys Phe His															
					180					185					190
Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser Lys Arg															
					195					200					205
Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys Met Pro															
					210					215					220
Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His Ala Gly															
					225					230					240
Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val															
					245					250					

<210> 72  
<211> 748  
<212> DNA  
<213> Secale cereale

<400> 72  
gtgcggaaag aggtcttaa actccttagag gcaggtatta actatccat tgctgata 60  
cagcggtaa gtcatgtcca ttgtgtccct aagaaaggag gtatgactgt cgtccctaag 120  
gataaaatgt aatttatccc gcaaagaata gttacaggtt ataggatgtt aattgatttt 180  
cgtaagttaa ataaagctac tatgaaagat cattaccct tgccatttat tgatcaaatg 240  
ccagacaggt tatccaaaca tactcattc tgcttctag atggttattc tggttctct 300  
caaataccctt tgtcaaagggg ggatcaagaa aagaccacct ttacttgtcc tttcggtacc 360  
tttgcttata gaggtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt 420  
atgatcgatgtt aattctctgtt ctttttggaa aagattgttg aggtattcat ggatgattc 480

tccgttatg gaacttctt tcatgtatgc ttaagcaacc ttgatcgagt tttgcagaga 540  
tgtgaagata ctaaccttgc cttgaattgg gagaagtgcc actttatggc taatgaaggc 600  
attttcttgg gacataaaaat ttctgaaaga ggtactgaag ttgagaaagc taaagtggat 660  
gctattgaaa agatgccatg ccctaaggat atgaaaggta tacgaagttt ccttggtcac 720  
gctgggtttt ataggaggtt cataaaaag 748

<210> 73  
<211> 249  
<212> PRT  
<213> Secale cereale

<400> 73  
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Asn Tyr Pro  
1 5 10 15  
  
Ile Ala Asp Ser Gln Arg Val Ser His Val His Cys Val Pro Lys Lys  
20 25 30  
  
Gly Gly Met Thr Val Val Pro Lys Asp Lys Asp Glu Phe Ile Pro Gln  
35 40 45  
  
Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
50 55 60  
  
Lys Ala Thr Met Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80  
  
Pro Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
85 90 95  
  
Ser Gly Phe Ser Gln Ile Pro Leu Ser Lys Gly Asp Gln Glu Lys Thr  
100 105 110  
  
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Gly Met Pro Phe  
115 120 125  
  
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ile Val Ile  
130 135 140  
  
Phe Ser Val Phe Phe Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160  
  
Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
165 170 175  
  
Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Phe Leu Gly His Lys Ile Ser  
195 200 205

Glu Arg Gly Thr Glu Val Glu Lys Ala Lys Val Asp Ala Ile Glu Lys  
210 215 220

Met Pro Cys Pro Lys Asp Met Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys  
245

<210> 74

<211> 762

<212> DNA

<213> Secale cereale

<400> 74

gtgcggaaagg aggtcgtaa gcttccagag gcaggtatta tctatcccgt tgctgatacg 60  
cagtggtaa gtcatgtcca ttgtgtccct aagaagggag gtatgactgt cgttccta 120  
gacaaacatg aattgatccc gcaaagaata gttacagggtt ataggatggt aattgatttc 180  
cgtaagttaa ataaagctac taagaaagat cattaccct tgccatttat tgatcaa 240  
ctagacaggt tatccaaaca tactcattt tgcttctag atggttatta tggttctct 300  
caaatacctg tgtcaaaagg gnatcaagaa aagaccactt tcacttgtcc tttcggtacc 360  
tttgcttata gacgtatgcc ttttggttt tgaatgcac ctgctacctt tcaaagatgt 420  
atgatggcta tattatctga tttttgagaa aagattgtt aggttttcat ggatgatttc 480  
tccgtttacg gaacctctt tcatgactac ttaagcaaca atgatcgagt tttgcagaga 540  
tgtgaagaca ctaatcttgc tttgaattgg gagaagtgcc actttatggt taatgaaggc 600  
attgtcttgg gacaaaaat ttctgaaaga ggtattgaag ttgacaaagc taaagtcgat 660  
gctggtgaaa agatgccatg ccccaaggac atcaaaggta tacgaagttt cttggcgtcat 720  
gttggggtttt ataggaggtt catcaaagac ttcacgaaag tt 762

<210> 75

<211> 254

<212> PRT

<213> Secale cereale

<400> 75

Val Arg Lys Glu Val Val Lys Leu Pro Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Ala Asp Ser Gln Trp Val Ser His Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Pro Asn Asp Lys His Glu Leu Ile Pro Gln

35

40

45

Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn		
50	55	60
Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met		
65	70	75
Leu Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr		
85	90	95
Tyr Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr		
100	105	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe		
115	120	125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile		
130	135	140
Leu Ser Asp Phe Glx Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe		
145	150	155
Ser Val Tyr Gly Thr Ser Phe Asp Asp Tyr Leu Ser Asn Asn Asp Arg		
165	170	175
Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly Gln Lys Ile Ser		
195	200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys		
210	215	220
Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His		
225	230	235
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

&lt;210&gt; 76

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Secale cereale

&lt;400&gt; 76

gtgcgtaagg aggtggtaa gctcctagaa gcaggtatta tctatccagt tgctgatagt 60  
cagtggtaa gtcatgtcca ttatgttctt aagaaaaggag gtatgactgt tgcctaat 120  
gataaaagatg aattgatccc gcaaagaata gttacaggtt ataggatggt aagtgattc 180  
cgtaagttga ataaagccac taagaaagat cattaccct tgccatttat tgcataatg 240  
ctagaaaagt tatccaaaca tactcattc ttcttcttag atggtttattc tggtttctct 300  
caaatacctg tgtcaaaaagg ggatcaagaa aagaccacct ttacttgac tttcggtacc 360  
tttgcttata gacgtatgcc tttggttta tgtaatgcac ctgctacctt tcaaagatgc 420  
atgatggcta tattctctga ctttgtgaa aagattgtg aggtattcat ggatgattc 480  
tccgttacg gaaccttctt tcatgattgc ttaagcaacc ttgatcgagt tttgcagaga 540  
tgtgaagaca ctaaccttgt cttgaattgc gagaagtgcc actttatggt taatgaaggc 600  
attgtcttgg gacataaaat ttctgaaata ggtattgaag ttgacaaagc taaagttgat 660  
gctattgaaa agatgccatg cgcaaaggac atcaaaggta tacggagttt cttggcat 720  
gccgggtttt ataggaggtt catcaaagat ttctcaaagg tt 762

<210> 77

<211> 254

<212> PRT

<213> Secale cereale

<400> 77

Val Arg Lys Glu Val Val Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Ala Asp Ser Gln Trp Val Ser His Val His Tyr Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
35 40 45

Arg Ile Val Thr Gly Tyr Arg Met Val Ser Asp Phe Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ser Lys His Thr His Phe Phe Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Thr Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
  
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
  
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Cys Glu Lys  
 180 185 190  
  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
  
 Glu Ile Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220  
  
 Met Pro Cys Ala Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 78  
 <211> 759  
 <212> DNA  
 <213> Secale cereale

<400> 78  
 gtgcgcagg aagttttaa gtttctagag gcaggtataa tctatccagt tgctgatagc 60  
 cagtggtaa gtcctgtcca ttgtgtccct aagaaggtag gtatgactgt agttccta 120  
 gataaagatg aattgatctc gcaaagaatt gttacaggtt ataggatggt aattgatttt 180  
 cgcaaattaa ataaagccac taagaaagat caataccctt tgccctttat tgcataatg 240  
 cttagaaaggt tatccaaaca cacccatttt tgcttctag atggttattc tagttctct 300  
 caaataccta tgtcaaaagg ggataaagaa aagaccactt ttacttgtcc ctttgtact 360  
 ttgcttatag acgtatgcct tttggtttat gtaatgcatt tgctaccctt caaacatgca 420  
 tgcataatgactctatgat ttttgtaaaa gaatgttgat gtttcatgg atgattttg 480  
 tatttacgaa acttctttg atgattgctt gagcaacctt gatcgagtt tgcagagatg 540  
 tgaagaaaact aatcttgtct tgaactggaa aaagtcccac tttatggta atgaaggcat 600  
 tgcttgggac ataaaatttc taaaagaggt accgaagttg acaaagctaa agttgatgct 660  
 gttgaaaaga tgccatgtcc caaggacatc aaaggtataa gaagttcct tggcatgcc 720  
 gggtttataa ggaggtttat caaggactc accaagggtt 759

<210> 79  
 <211> 254  
 <212> PRT  
 <213> Secale cereale

<400> 79

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Ala Asp Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Ser Gln  
35 40 45

Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp Gln Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Ser Phe Ser Gln Ile Pro Met Ser Lys Gly Asp Lys Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Ser Ala Thr Phe Gln Thr Cys Met Met Ala Ile  
130 135 140

Leu Tyr Asp Phe Cys Glu Arg Ile Val Asp Val Phe Met Asp Asp Phe  
145 150 155 160

Cys Ile Tyr Glu Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Ser His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Glu Arg Gly Thr Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys  
210 215 220

Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 80  
<211> 761  
<212> DNA  
<213> *Triticum aestivum*

<400> 80  
gtgcgtaagg aggttctcaa gtttctggag gtaggtataa tttatcccgt tgctgatagt 60  
cagtggtaa gtcctgtcca ttgtgtccct aagaaggag gtattactgt tgtcccta 120  
gataaaagatg aattgattcc tcaaagaatt attacggta taggatggta attgattcc 180  
gcaaattaaa taaagccact aagagagatc attaccctt accttttatt gatcaaattc 240  
tagaaagatt atgcaaacat acacattatt gctccaaga tggttatcct ggttttctc 300  
aaatacctgt gtcggctaaa gatcaatcaa agactactt tacatgccct tttggta 360  
ttgcttataag atgtatgcct tttggtttat gtaatgcacc tgctaccctt caaagatgca 420  
tgatggctat attctctgat ttttgtaaa agattgtga gggtttcatg gatgacttt 480  
ccgtctatgg ttccctttt gatgattgct tgagcaatct tgatcgagtt ttgcagagat 540  
gtgaagaaac taatcttgc ttgaattggg aaaagtgtca ctttatggtt aatgaaggta 600  
ttgtcttggg gcacaaagtt tctgaaagag gtattgaagt tgataaagcc aagggtgaca 660  
ctattgaaaa gataccatgt cccaggaca tcaaaggta aagaagttc ctggtcacg 720  
ccggattttta taggaggttc ataaaagatt tcacaaagg 761

<210> 81  
<211> 254  
<212> PRT  
<213> *Triticum aestivum*

<400> 81  
Val Arg Lys Glu Val Leu Lys Phe Leu Glu Val Gly Ile Ile Tyr Pro  
1 5 10 15

Val Ala Asp Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Arg Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Ile  
65 70 75 80

Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Gln Asp Gly Tyr  
85 90 95

Pro Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr

100	105	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe		
115	120	125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile		
130	135	140
Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe		
145	150	155
Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg		
165	170	175
Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser		
195	200	205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Thr Ile Glu Lys		
210	215	220
Ile Pro Cys Pro Lys Asp Ile Lys Gly Thr Arg Ser Phe Leu Gly His		
225	230	235
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 82  
 <211> 780  
 <212> DNA  
 <213> Triticum aestivum

<400> 82  
 gtgcggaagg aggtgtttaa gtccttgag gcaggtataa ttatccgt tgctgatagt 60  
 aagtggtaa ttcctgtcca ttaagtgatc gtgattactg ttgtcctaa gaaggaggt 120  
 attaccgttgc ttccatatga taaagatgaa ttgattcctc aaagaaccat tactggttat 180  
 agatggtaa ttgattccg caaattaaat aaggctacta aaaaatatca ttacccctta 240  
 cctttatcg atcaaatgct agaaagatta tccaaacata cacatcccc 300  
 gtttactctg gtttctctca aataccgttg tcagccaaag atcaatcaa gactactttt 360  
 acatgccctt ttggacttt tgcttataga cgtatgcctt ttggttatg taatgcacct 420  
 gtttcatgg acgactcttc catctatgaa tcttctttt atgattgctt gagcaacctt 480  
 gatcgagtt tgcagagatg tgaagaaact tatcttgtct tgaattggaa aaagtgccaa 540  
 tttatggta atgaaggtat tgtcctgggg cataaaagttt ctgaaagagg tattcgagtt 600  
 gataaaagcca aggttgatgc tattgaaaag atgccatgct ccatggacat caaaggtata 720

agaagtttcc ttggcatgc cggttttat aggaggttca taaaagactt cacgaagg 780

<210> 83  
<211> 260  
<212> PRT  
<213> Triticum aestivum

<400> 83

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	

Val Ala Asp Ser Lys Trp Val Ile Pro Val His Glx Val Ile Val Ile

20				25					30						
----	--	--	--	----	--	--	--	--	----	--	--	--	--	--	--

Thr Val Val Pro Lys Lys Gly Gly Ile Thr Val Val Pro Asn Asp Lys

35				40					45						
----	--	--	--	----	--	--	--	--	----	--	--	--	--	--	--

Asp Glu Leu Ile Pro Gln Arg Thr Ile Thr Gly Tyr Arg Met Val Ile

50				55					60						
----	--	--	--	----	--	--	--	--	----	--	--	--	--	--	--

Asp Phe Arg Lys Leu Asn Lys Ala Thr Lys Lys Tyr His Tyr Pro Leu

65				70					75					80	
----	--	--	--	----	--	--	--	--	----	--	--	--	--	----	--

Pro Phe Ile Asp Gln Met Leu Glu Arg Leu Ser Lys His Thr His Phe

85				90					95						
----	--	--	--	----	--	--	--	--	----	--	--	--	--	--	--

Cys Phe Leu Asp Gly Tyr Ser Gly Phe Ser Gln Ile Pro Val Ser Ala

100				105					110						
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	--	--

Lys Asp Gln Ser Lys Thr Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala

115				120					125						
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	--	--

Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln

130				135					140						
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	--	--

Arg Tyr Met Met Ala Ile Leu Ser Asp Phe Cys Glu Lys Ile Cys Glu

145				150					155					160	
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	-----	--

Val Phe Met Asp Asp Ser Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys

165				170					175						
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	--	--

Leu Ser Asn Leu Asp Arg Val Leu Gln Arg Cys Glu Glu Thr Tyr Leu

180				185					190						
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	--	--

Val Leu Asn Trp Glu Lys Cys Gln Phe Met Val Asn Glu Gly Ile Val

195				200					205						
-----	--	--	--	-----	--	--	--	--	-----	--	--	--	--	--	--

Leu Gly His Lys Val Ser Glu Arg Gly Ile Arg Val Asp Lys Ala Lys  
210 215 220

Val	Asp	Ala	Ile	Glu	Lys	Met	Pro	Cys	Pro	Met	Asp	Ile	Lys	Gly	Ile
225				230						235					240

Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp  
245 250 255

Phe Thr Lys Val  
260

<210> 84  
<211> 762  
<212> DNA  
<213> *Triticum aestivum*

<400> 84  
gtgcgttaagg aggtattcaa gcttctggag gcaggtataa tttatcccgt tgttgatagt 60  
caatgggtaa gtccgtccta ttgtgtcctt aagaagggag gtattactgt tgtccctaata 120  
gataaaagatg aattgattcc gcaaagaatt atcacaggtt ataggatggt aattgatttc 180  
cgtaagttaa ataaagctac taagaaagat cattaccctt tacctttat tgatcaaatg 240  
ttagaaagat tatgcaaaca tacacattat tgctttctag atggttattc tggttctct 300  
caaataacctg tgcagctaa ggtcaatca aagactactt ttacatgccc ttttgttact 360  
tttgttata gacgtatgcc ttgcattta tgtaatgcac ctgctacctt tcaaatatgc 420  
atgatggcta tattctctga ctttgcgaa aagatttg aggtttcat ggacgacttt 480  
tccgtctatg gtcctctta tgatgattgc ttgagcaatc ttaatcgagt tttgcagaga 540  
tgtgaagaaa ctaatcttgc cttgaattgg gaaaagtgc actttatggt taatgaaggt 600  
attgtcttgg ggcacaaaagt ttctgaacga ggtattgaag ttgataaggc caaggttgat 660  
gctattgaaa agatgacatg tcccaaggac atcaaaggta taagaagttt cttggtcac 720  
gccagattt ataggagggtt cataaaagac ttcacaaagg tt 762

<210> 85  
<211> 254  
<212> PRT  
<213> *Triticum aestivum*

<400> 85  
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Val Asp Ser Gln Trp Val Ser Pro Val His Cys Val Leu Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
 50 55 60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80

Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95

Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr  
 100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Gly Tyr Arg Arg Met Pro Phe  
 115 120 125

Asp Leu Cys Asn Ala Pro Ala Thr Phe Gln Ile Cys Met Met Ala Ile  
 130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe  
 145 150 155 160

Ser Val Tyr Gly Ser Ser Tyr Asp Asp Cys Leu Ser Asn Leu Asn Arg  
 165 170 175

Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220

Met Thr Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240

Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 86  
 <211> 762  
 <212> DNA  
 <213> Triticum aestivum

<400> 86  
 gtgcggaaag aggtgctcaa gcttctggag gcaggtataa tttatccgt tgctgagagt 60

cagtggtaa gtcctgtcca ttgtgtccct aagaagggag gtattactgt tgtcccta 120  
gataaaagatg aattgattcc tcaaagaatt attacagggtt ataggatggt aattgattc 180  
cgcaaaattaa ataaaagccac caagaaagat cattaccct tacctttat tgatcaaatg 240  
ctagaaagat tatgcaaaca tacacattat tgcttcctag atggttattc tggttctct 300  
caaatacctg tgccggctaa agatcaatca aagactactt ttacatgccc tttggta 360  
tttgcttata gacgtatgcc ttttggtta tgtaatgcac cttctacctt tcaaagatgc 420  
atgatggcta tattctctga ttttgtgaa aagatttg aggtttcat ggacgaattt 480  
tccgtctatg gttcctctt tgatgattgc ttgagcaatc ctgatcgagt ttgcagaga 540  
tgtgaagaaa ctaatcttgc cttgaattgg gaaaagtgc actttatggtaatgaaggt 600  
attgtcttgg ggcacaaagt ttctgaaaga ggtattgaag ttgataaagc caagggtgac 660  
gctattgaaa agatgccatg tccccaggac atcaaaggta taagaagttt ccttggcac 720  
gccggatttt ataggagggtt cataaaagac ttcaccaaagg tt 762

<210> 87

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 87

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Ala Glu Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ser Thr Phe Gln Arg Cys Met Met Ala Ile  
130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Glu Phe

145

150

155

160

Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Pro Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
210 215 220

Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 88

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 88

gtgcgttaagg aggtttcaa gttcctttag gcaggttata cttatccgt tgctgatagt 60  
gaatggtaa gcccttcctt ttgtgttcctt aaaaaggtag gtattaccgt tggcttaat 120  
gataaaagatg aatttgcattt gcaaaataattt attacagggtt ataggatgggt aatttgcattt 180  
cataagttaa ataaagctac taagaaagat cattaccctt tacctcttat tgatcaaatt 240  
ctagaaaagac tatccaaaca cacacattt tgctttcttag atggttatac tggtttctct 300  
caaatacctg tgtcagtgaa ggatcaatct aaaactactt ttacttgccc ttttggtaact 360  
tttgcttata gacttatgcc ttttggttta tgtaatgcac ctacttcctt tcaaagatgc 420  
atgtatggctta tatttcttgtt tttttgtgaa aatatttgcgtt aggtattcat ggatgatttc 480  
tccgtttatg gatcctcttt tgatgatgtt ttgagcaacc ttgatcgagt tttgcagaga 540  
tgcgaaagaca ctagtctcat cctgaattgg gaaaaagtgtc actttatgggt taatgaaggc 600  
attgtcttgg ggcataagat ttccgagaga ggtattgaag ttgacaaagc caaagttgat 660  
gctattgaaa agattccatg tccccaggac ataaaaggta taagaagttt cttggatcat 720  
gctggttttt ataggaggtt catcaaagac ttctcaaagg tt 762

<210> 89

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 89

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Thr Tyr Pro  
1 5 10 15

Val Ala Asp Ser Glu Trp Val Ser Pro Leu His Cys Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Leu Asn Asp Lys Asp Glu Leu Ile Pro Gln  
35 40 45

Ile Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe His Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Leu Ile Asp Gln Ile  
65 70 75 80

Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Thr Gly Phe Ser Gln Ile Pro Val Ser Val Lys Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Leu Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Thr Ser Phe Gln Arg Cys Met Met Ala Ile  
130 135 140

Phe Ser Val Phe Cys Glu Asn Ile Cys Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Asp Thr Ser Leu Ile Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
210 215 220

Ile Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
245 250

<210> 90  
<211> 791  
<212> DNA  
<213> Gossypium hirsutum

<400> 90

gtgcgcagg aggtttaaa gctacttgat gacgggatga tctatcccat atctaacagt 60-  
aattgggta gcccagtaca catagtagcca aaaaagacca gtgcaaccgt aatcgagaat 120  
tcggcagggtg agatagttcc cactcgggtc caaaacgggt ggagagttatg catcgattac 180  
aggaagttga attccttaac tcggaaggat cacttccac ttccctttat tgaccagatg 240  
ttagaacgtt tagctggaaa gtctcattat ttagaacgtt tagctggaaa gtctcattat 300  
tgttgggg atggttacta aggttttc cagatcccag tggcaccgga ggtcaagaa 360  
agacaatgtt tacgtgccca tttggcacgt tttcttacag acggatgccc ttcggactct 420  
gtaatgcacc agccagttt cataggtgca tggtaagtat atttcagac tacgtcgata 480  
aaattatcga ggtgttcatg gacgacttta ctgttatatgg tgagtccctc gaggttaagtc 540  
tgacgaacct tgcaaaaatt ttggaaagat gcttagaatt taatcttgc ttcaaattatg 600  
agaaaatgcca ttttatggta gacaaggat tagttctagg tcatattatt tctgctgatg 660  
gaatttctgt tgataaaagca aaaatcaaca tcattaaactc actaccatac cccacaactg 720  
tgagggagat ttggtcttcc cttggtcatg caggttcta caagtgggatc atcaaagact 780  
tttcaaaaagt t 791

<210> 91  
<211> 264  
<212> PRT  
<213> Gossypium hirsutum

<400> 91

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Asp Gly Met Ile Tyr Pro  
1 5 10 15

Ile Ser Asn Ser Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys  
20 25 30

Thr Ser Ala Thr Val Ile Glu Asn Ser Ala Gly Glu Ile Val Pro Thr  
35 40 45

Arg Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Ser Leu Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Lys Ser His Tyr Leu Glu Arg Leu Ala Gly  
85 90 95

Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr Glx Gly Phe Phe Gln Ile

100	105	110
Pro Val Ala Pro Glu Asp Gln Glu Lys Thr Met Phe Thr Cys Pro Phe		
115	120	125
Gly Thr Phe Ser Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro		
130	135	140
Ala Ser Phe His Arg Cys Met Val Ser Ile Phe Ser Asp Tyr Val Asp		
145	150	155
Lys Ile Ile Glu Val Phe Met Asp Asp Phe Thr Val Tyr Gly Glu Ser		
165	170	175
Phe Glu Val Ser Leu Thr Asn Leu Ala Lys Ile Leu Glu Arg Cys Leu		
180	185	190
Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys Cys His Phe Met Val Asp		
195	200	205
Lys Gly Leu Val Leu Gly His Ile Ile Ser Ala Asp Gly Ile Ser Val		
210	215	220
Asp Lys Ala Lys Ile Asn Ile Ile Asn Ser Leu Pro Tyr Pro Thr Thr		
225	230	235
Val Arg Glu Ile Trp Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Trp		
245	250	255
Phe Ile Lys Asp Phe Ser Lys Val		
260		

<210> 92  
 <211> 763  
 <212> DNA  
 <213> *Gossypium hirsutum*

<400> 92  
 gtgcgtaaaag aggtcgtaaa gctacttgat tccggatga tctatcccat atctgacaat 60  
 aattgggta gtccagtcca catagtaccc aaaaagaccg gtgttaaccgt aattgagaat 120  
 tcagcagggtg agatggttcc cacttaagtc cgaaacggtc ggagagtagatg catcgattac 180  
 aggaagttga attcctaac tcggaaagat cacttccac ttcttttat tgatcagatg 240  
 ttagaacatt tagccagaaa gtctcattat tgttgtctgg atggttactc aggtttttc 300  
 cagatcccaa tggcactaaa ggatcaagaa aagatgacat ttacgtgccc atttggcatg 360  
 ttgcgttata gaaggatgtc gtttcagact ttgcaatgca ccaaccatgt ttcagaggtg 420  
 catgataagt atatttttg actatgttaa gaaaataatt gaggtgttca tggacgaatt 480  
 tactgtatat agttagtcct tcgaggatata tttgtcaat ctagaaaaat ttttggaaag 540

atgcttagaa tttaatcttg ttctaaatatta tgagaattgc tatttaatgg tagacaaggg 600  
attagttcta ggtcatatca tttctgctaa gggaaatttct gtcgataaaag taaaaattaa 660  
catcataagc tcaataccat accccacaaac tgtgagggag attcggttctt tccttagtca 720  
tatagtttc tataggcgat tcatcaagga cttttcaaaa gtt 763

<210> 93  
<211> 254  
<212> PRT  
<213> Gossypium hirsutum

<400> 93  
Val Arg Lys Glu Val Val Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro  
1 5 10 15  
  
Ile Ser Asp Asn Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys  
20 25 30  
  
Thr Gly Val Thr Val Ile Glu Asn Ser Ala Gly Glu Met Val Pro Thr  
35 40 45  
  
Glx Val Arg Asn Gly Arg Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60  
  
Ser Leu Thr Arg Lys Asp His Phe Pro Leu Leu Phe Ile Asp Gln Met  
65 70 75 80  
  
Leu Glu His Leu Ala Arg Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr  
85 90 95  
  
Ser Gly Phe Phe Gln Ile Pro Met Ala Leu Lys Asp Gln Glu Lys Met  
100 105 110  
  
Thr Phe Thr Cys Pro Phe Gly Met Phe Ala Tyr Arg Arg Met Ser Phe  
115 120 125  
  
Arg Leu Cys Asn Ala Pro Thr Met Phe Gln Arg Cys Met Ile Ser Ile  
130 135 140  
  
Phe Phe Asp Tyr Val Lys Lys Ile Ile Glu Val Phe Met Asp Glu Phe  
145 150 155 160  
  
Thr Val Tyr Ser Glu Ser Phe Glu Val Tyr Leu Ser Asn Leu Glu Lys  
165 170 175  
  
Phe Leu Glu Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Asn  
180 185 190

Cys Tyr Leu Met Val Asp Lys Gly Leu Val Leu Gly His Ile Ile Ser  
195 200 205

Ala Lys Gly Ile Ser Val Asp Lys Val Lys Ile Asn Ile Ile Ser Ser  
210 215 220

Ile Pro Tyr Pro Thr Thr Val Arg Glu Ile Arg Ser Phe Leu Ser His  
225 230 235 240

Ile Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
245 250

<210> 94

<211> 723

<212> DNA

<213> Gossypium hirsutum

<400> 94

gtgcgtaagg aggtttgaa attgttggat gctggaatga tataactcgat ctttgacagt 60  
gattgggtta gctgggttca tgtcgtgcc aaaaaactg gcgtgacagt ggtgaaaac 120  
tcatcaggag agctagtccc tacccgagtc cagaatcgat ggaggggttg catcgattac 180  
aggaagttga acgcagctac ccgaaatgac cattttccac ttcccttcat tgatcaaatg 240  
ctcgagcgat tagctaataa gaccattat tgttgtctcg atgggtactc aggactttc 300  
caaattccgg tggcacctga gnatcaagac aaaacaacct tcacgtgcc ctttggaaacg 360  
tttgcgtata gaagaatgtc gtttggactc tgtaatgctc cggccacttt ccagagatgt 420  
atggtgagca tattctctga ttatgtcgag aaaatcattt aattcttcat gnatgacttc 480  
acgggtgtacg gtaactctt taacgaatgt ctgcataatc ttgctaagat attacagaga 540  
tgcctagaat ttaatcttgt tttaaattat gaaaaatgcc acttcatggg tgacaaagga 600  
ttaattttgg gtcataatgt ttottcagaa ggtattgagg tcaataaagc aaaaacgaat 660  
attattgact cattacctt ccccagattt tacagacgat tcataaaagga cttcacaaaa 720  
gtt 723

<210> 95

<211> 241

<212> PRT

<213> Gossypium hirsutum

<400> 95

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Gly Met Ile Tyr Ser  
1 5 10 15

Ile Phe Asp Ser Asp Trp Val Ser Trp Val His Val Val Pro Lys Lys  
20 25 30

Thr Gly Val Thr Val Val Lys Asn Ser Ser Gly Glu Leu Val Pro Thr  
35 40 45

Arg Val Gln Asn Arg Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn  
               50                         55                         60

Ala Ala Thr Arg Asn Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
       65                         70                         75                 80

Leu Glu Arg Leu Ala Asn Lys Thr His Tyr Cys Cys Leu Asp Gly Tyr  
       85                         90                         95

Ser Gly Leu Phe Gln Ile Pro Val Ala Pro Glu Asp Gln Asp Lys Thr  
       100                        105                        110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe  
       115                        120                        125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile  
       130                        135                        140

Phe Ser Asp Tyr Val Glu Lys Ile Ile Glu Phe Phe Met Asp Asp Phe  
       145                        150                        155                 160

Thr Val Tyr Gly Asn Ser Phe Asn Glu Cys Leu Asp Asn Leu Ala Lys  
       165                        170                        175

Ile Leu Gln Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys  
       180                        185                        190

Cys His Phe Met Val Asp Lys Gly Leu Ile Leu Gly His Ile Val Ser  
       195                        200                        205

Ser Glu Gly Ile Glu Val Asn Lys Ala Lys Thr Asn Ile Ile Asp Ser  
       210                        215                        220

Leu Pro Tyr Pro Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys  
       225                        230                        235                 240

Val

<210> 96

<211> 762

<212> DNA

<213> Lycopersicon esculentum

<400> 96

gtgcggaaag aggttgtgaa gctgttagat acgggtattg tctagccaat ttccggacaac 60

aagttaggtta gtccagtaca atgtgaacct aaaaagggag acataacggt gatcactaat 120  
gaaaaaaaaatg agttgatccc aaccatgata gtcacataat ggagaatatg catggattac 180  
aggaaattga atgaagccac caggaaggac cattaccgg tccctttat tgatcagatg 240  
ttggaccggt tggctgggaa ataatattat tggttctta atggctattt acggtacaac 300  
caaattgtga tttcaccaaa ggattaagag aaaaccactt tcacttgccc gtatggtaca 360  
tatgcttca aaaagatacc ttttgggta tgaaatgcct cggtacttt ccaatgatgc 420  
atgatggcta ttttcatga tatggttgaa gatggttg agatattcat gaatgatttc 480  
tcagtgttg gggattctt tgatatgtgc ttggagaatt tggacagtgt gtggctagt 540  
tgtgaagaaa ctaatcttt cctaaaactgg gaataatagc aatttctagt aaaggaaggg 600  
attatgctag gacataaggt gtcaaagaga ggtatggaag ttgatagtgc caaagtggag 660  
gttattgaaa agctcccccc tcctatatct gttaaaggga tgcaaagttt tctgggtcat 720  
gttgggttct ataggagatt cataaaagac ttcacaaagg tt 762

<210> 97

<211> 254

<212> PRT

<213> Lycopersicon esculentum

<400> 97

Val Arg Lys Glu Val Val Lys Leu Leu Asp Thr Gly Ile Val Glx Pro  
1 5 10 15

Ile Ser Asp Asn Lys Glx Val Ser Pro Val Gln Cys Glu Pro Lys Lys  
20 25 30

Gly Asp Ile Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
35 40 45

Met Ile Val Thr Glx Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Asp Arg Leu Ala Gly Glu Glx Tyr Tyr Cys Phe Leu Asn Gly Tyr  
85 90 95

Leu Arg Tyr Asn Gln Ile Val Ile Ser Pro Lys Asp Glx Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Lys Ile Pro Phe  
115 120 125

Gly Leu Glx Asn Ala Ser Ala Thr Phe Gln Glx Cys Met Met Ala Ile  
130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asn Asp Phe

145

150

155

160

Ser Val Phe Gly Asp Ser Phe Asp Met Cys Leu Glu Asn Leu Asp Ser  
165 170 175

Val Leu Ala Ser Cys Glu Glu Thr Asn Leu Phe Leu Asn Trp Glu Glx  
180 185 190

Glx Gln Phe Leu Val Lys Glu Gly Ile Met Leu Gly His Lys Val Ser  
195 200 205

Lys Arg Gly Met Glu Val Asp Ser Ala Lys Val Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Ile Ser Val Lys Gly Met Gln Ser Phe Leu Gly His  
225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 98

<211> 689

<212> DNA

<213> Lycopersicon esculentum

<400> 98

cgaaaggagg tggtaaaact ggaaattatc aagtagttgg atgctagagt aatctatcca 60  
atcgccgata gtagttgggt atgcctagtt cagtggtac caaagaaaagg gggaatgact 120  
gtggtccccca acgaaaagaa tgaacttgtt cgaatgagac cggttactgg atggagggtg 180  
tgcattggatt accgtaaact gaactcatag actaaaaaag actatttca tatgcccttc 240  
atggatcaga tggatggatag acttgccgga aaagggtggg attgtttct tggatggat 300  
tcggggatata atcagatttc tattgcacca gaagatcaag agaaaaccac tttcacttgt 360  
ccatacggga ctttgcatt cagaagaatg tcgtttgggt tgtgcaatgc acccgcaacc 420  
tttcagagat ggatgatgtc aatattttct gacatgatgg aggataactat agagggtttt 480  
atggatgatt ttctgtggg tggatgttca ttgcagcggt gcttgcacaa ttatctgag 540  
gttcttaaga gatgtgaaga ctgcaatttg gtactaaact gggaaaagtg tcatttcatg 600  
gtgaaagagg gtattgtgtt gggatcgatc atttcagaaa agggcatgca tggttttact 660  
ggatcatcaa acaagacttc acaaaagg 689

<210> 99

<211> 229

<212> PRT

<213> Lycopersicon esculentum

<400> 99

Arg Lys Glu Val Val Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala Arg

1

5

10

15

Val Ile Tyr Pro Ile Ala Asp Ser Ser Trp Val Cys Leu Val Gln Cys  
20 25 30

Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Glu Lys Asn Glu  
35 40 45

Leu Val Arg Met Arg Pro Val Thr Gly Trp Arg Val Cys Met Asp Tyr  
50 55 60

Arg Lys Leu Asn Ser Glx Thr Glu Lys Asp Tyr Phe His Met Pro Phe  
65 70 75 80

Met Asp Gln Met Leu Asp Arg Leu Ala Gly Lys Gly Trp Tyr Cys Phe  
85 90 95

Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ser Ile Ala Pro Glu Asp  
100 105 110

Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Arg  
115 120 125

Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Trp  
130 135 140

Met Met Ser Ile Phe Ser Asp Met Met Glu Asp Thr Ile Glu Val Phe  
145 150 155 160

Met Asp Asp Phe Ser Val Val Gly Asp Ser Phe Glu Arg Cys Leu Ser  
165 170 175

Asn Leu Ser Glu Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu  
180 185 190

Asn Trp Glu Lys Cys His Phe Met Val Lys Glu Gly Ile Val Leu Gly  
195 200 205

His Arg Ile Ser Glu Lys Gly Met His Val Phe Thr Gly Asp Ser Ser  
210 215 220

Lys Thr Ser Gln Arg  
225

<210> 100  
<211> 760  
<212> DNA

<213> Lycopersicon esculentum

<400> 100

gtgcgtaagg aggtgtttaa gcttctagat gcgggtattg tctacccaat taggacaaca 60  
agtgggttag tctagtacaa tgtgtaccta aaaagggagg catggcaatg attactaatg 120  
aaaacaatga gtttatccca accagcacag tcacaagatg gcgaatatgc atgaattaca 180  
cgaagttaat gaagccacta ggaagaatca ttacccaatt ctttttattg attatatgtt 240  
ggaccggtaa gctggcaag aatattattt ttttttgat tactaatcag ggtacaacta 300  
aattttgatt gcaccagagg atcaagagaa aacaacttc acttgcggcg atggatcata 360  
tgcttcaga aggatacctt ttgggttatg caatgctcg tctaattcc aaagatgcat 420  
gatgactatt tttcatgata tggttgaata ttttgaggat atattcatgg atgatttctt 480  
agtgtttgg gagtcgtttg atagatgctt ggagaattt aacaggttgt tagcttaggtg 540  
cgaacaaact aatcttgc tgaactggaa aaaatgtcat ttttagtaa aggaaggaa 600  
ttttcgggg cataaggtgt aaaagatagg gctggaagtt gatcatgaca aagtggaagt 660  
aattgaaaag atctcccttc ccattttgt gaaacgggtg agaagttac taggtcatgc 720  
tgagtttac aggatattca tcaaggactt ctcaaagggtt 760

<210> 101

<211> 254

<212> PRT

<213> Lycopersicon esculentum

<400> 101

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro  
1 5 10 15

Ile Ser Asp Asn Lys Trp Val Ser Leu Val Gln Cys Val Pro Lys Lys  
20 25 30

Gly Gly Met Ala Met Ile Thr Asn Glu Asn Asn Glu Phe Ile Pro Thr  
35 40 45

Ser Thr Val Thr Arg Trp Arg Ile Cys Met Asn Tyr Thr Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asn His Tyr Pro Ile Leu Phe Ile Asp Tyr Met  
65 70 75 80

Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Tyr Glx  
85 90 95

Ser Gly Tyr Asn Glx Ile Leu Ile Ala Pro Glu Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Ile Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Leu Ser Asn Phe Gln Arg Cys Met Met Thr Ile  
 130 135 140  
  
 Phe His Asp Met Val Glu Tyr Phe Glu Asp Ile Phe Met Asp Asp Phe  
 145 150 155 160  
  
 Leu Val Phe Trp Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asn Arg  
 165 170 175  
  
 Leu Leu Ala Arg Cys Glu Gln Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
  
 Cys His Phe Leu Val Lys Glu Gly Asn Phe Ser Gly His Lys Val Glx  
 195 200 205  
  
 Lys Ile Gly Leu Glu Val Asp His Asp Lys Val Glu Val Ile Glu Lys  
 210 215 220  
  
 Ile Ser Ser Pro Ile Phe Val Lys Arg Val Arg Ser Leu Leu Gly His  
 225 230 235 240  
  
 Ala Glu Phe Tyr Arg Ile Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 102  
 <211> 776  
 <212> DNA  
 <213> Lycopersicon esculentum-

<400> 102  
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 cgatctccga tagtagttgg gtatgcccta ttcaagtgtgt acctaagaaa gggggatga 120  
 ctgtggtccc caataagaaa aatgaacttg ttctaattgag accggttact ggagggtggg 180  
 tgtgtatgga ttaccgtaaa ttaaatgcat ggactgaaaa agaccatttt cctatgccct 240  
 tcattggatca gatgttggat agacttgcgg aaaaagggtg gtactgtttt cttgatggat 300  
 agtcagggtta taatttagatt tctattgcac cagaagatca agagaaaacc acatttactt 360  
 gtccatatgg gaccttgca ttgaagagaa tgtcgtttgg gttgtgcaat gcaccgcaca 420  
 catttcacag atgtaaaaat gttgatattc ttgcacatgg tggatgatac tattgtatgt 480  
 tttatggatg attttctct tggatggtaa tcattcgaga ggtgtttgaa ccatttatct 540  
 gatgtcctta agagatgtga agactgcaat ttagtactaa attggggaaaa atgccacttc 600  
 atggtgaaaa aaggatttgt tttgggtcat cgcattccag aaaagggtcat agagggttcat 660  
 cgagctaaag tagaggtaat agagagactt cccccactat ctctgtaaaa ggtgtgagaa 720  
 gctttcttgg gcatgcaagt tttaccgga gattcatcaa agacttcaca aaagtt 776

<210> 103  
 <211> 258

<212> PRT

<213> Lycopersicon esculentum

<400> 103

Ala Glu Arg Ser Val Glx Thr Gly Ile Ile Lys Trp Leu Asp Ala Gly  
1 5 10 15

Val Ile Tyr Pro Ile Ser Asp Ser Ser Trp Val Cys Pro Ile Gln Cys  
20 25 30

Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Lys Lys Asn Glu  
35 40 45

Leu Val Leu Met Arg Pro Val Thr Gly Gly Trp Val Cys Met Asp Tyr  
50 55 60

Arg Lys Leu Asn Ala Trp Thr Glu Lys Asp His Phe Pro Met Pro Phe  
65 70 75 80

Met Asp Gln Met Leu Asp Arg Leu Ala Glu Lys Gly Trp Tyr Cys Phe  
85 90 95

Leu Asp Gly Glx Ser Gly Tyr Asn Glx Ile Ser Ile Ala Pro Glu Asp  
100 105 110

Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Leu Lys  
115 120 125

Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe His Arg Cys  
130 135 140

Lys Met Leu Ile Phe Phe Asp Met Val Asp Asp Thr Ile Asp Ala Phe  
145 150 155 160

Met Asp Asp Phe Ser Leu Val Gly Glu Ser Phe Glu Arg Cys Leu Asn  
165 170 175

His Leu Ser Asp Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu  
180 185 190

Asn Trp Glu Lys Cys His Phe Met Val Lys Lys Gly Ile Val Leu Gly  
195 200 205

His Arg Ile Pro Glu Lys Gly Ile Glu Val Asp Arg Ala Lys Val Glu  
210 215 220

Val Ile Glu Arg Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser  
225 230 235 240

Phe Leu Gly His Ala Ser Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr  
                  245                   250                   255

Lys Val

<210> 104  
<211> 761  
<212> DNA  
<213> *Solanum tuberosum*

<400> 104  
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aatgggtaa gtccagtaaa gtgtgtcccc aagaagggca gaatgacggt gttgactaat 120  
gagaagaatg aggtaatccc cacaagaaca gtgactgggt gacggatttgcatggactac 180  
atgaagttga acgacgccac cagaaaggac cattatcogg taccttcattgataaaaata 240  
ttggataggt tggcaggaca tgagtactat tggtttcttg gtgtctactc agggtacaat 300  
cagattgtta ttgcaataga ggacttaggtg aaaaccacct tcacccgttc gtatggcaca 360  
tatgcgttca agcacatgcc attcggcttg tgcaatgcc tggccacatt tcagagatgc 420  
atgttggcaa tcttccatga tatggtggag gattttgttg aagtttcattgatgacttc 480  
ttggtgtttg gtgagtcttt tgaaccttgc ttgactaatt ttgacagatt tcttgcgttgc 540  
tgtgaagaga cgaatctggat gataaaactga tagaaagtgtc actttctggat tcgagagggaa 600  
attgtgttgg gacacaagat ctccaaaaat gggctgaaag ttgacaaagc caacgttagag 660  
gttattgaga aattgccacc cccatcacag tgaaggtaat taaaagcttac taggacatg 720  
cttggttta tacgagggttc atcaaagact tcacaaaggat t 761

<210> 105  
<211> 254  
<212> PRT  
<213> *Solanum tuberosum*

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<400> 105
Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Arg Ile Val Tyr Pro
      1           5           10          15

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Ile Ser Asp Ser Lys Trp Val Ser Pro Val Lys Cys Val Pro Lys Lys  
20 25 30

Arg Thr Val Thr Gly Glx Arg Ile Cys Met Asp Tyr Met Lys Leu Asn  
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Lys Ile

65

70

75

80

Leu Asp Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Gly Val Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Val Ile Ala Ile Glu Asp Glx Val Lys Thr  
100 105 110

Thr Phe Thr Cys Ser Tyr Gly Thr Tyr Ala Phe Lys His Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Leu Ala Thr Phe Gln Arg Cys Met Leu Ala Ile  
130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Leu Val Phe Gly Glu Ser Phe Glu Leu Cys Leu Thr Asn Phe Asp Arg  
165 170 175

Phe Leu Ala Arg Cys Glu Glu Thr Asn Leu Val Ile Asn Glx Glx Lys  
180 185 190

Cys His Phe Leu Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Lys Asn Gly Leu Lys Val Asp Lys Ala Asn Val Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Ile Thr Val Lys Val Ile Lys Ser Leu Leu Gly His  
225 230 235 240

Ala Trp Phe Tyr Thr Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 106

<211> 760

<212> DNA

<213> Solanum tuberosum

<400> 106

gtgcgtaaag aggtttcaa actgctagat gtcggtattg tatatccat ttcagaaaac 60  
aatgggtca gcccagttt gtgtgtgcct aaaaaaagag gcatgccgt gatcaccaat 120  
aaaaaaaaatg agttgattcc aaccaggaca gtgacagggt ggcgaatatg catggattat 180  
aggaaattga atgaggccac cagaaaggat cactgccccg ttcctttat tgatcagatg 240  
ctggacaggt tagtggcga agaatattat tgttcctgg aaggctattc aggataacaac 300  
caaattgtga ttgcaccaga ggaccaggag aaaactacat tcacttgtct gtatggaca 360

tatgcttc a gtgactgcc gtttggcta tgcaatgctc cagccaccc ttccaaagatga 420  
atgatggcta tcttcatga tatgggtgaa gattttgtgg agatattcat ggatgacttc 480  
tcagtctta gggagtctt tgataggtgt ttggagaatt gggacagggt gctggctaga 540  
tgcgaggaaa ctaatctcat cctaaactgg aaaaaatgtc atttcctagt aaatgaaggg 600  
attgtattgg gccataaggt gtcaaagaga gggctgaaag ttgatcgtgc caaagtggaa 660  
gttattgaaa aactacctcc tccaatctgt taaaggggtg agaagcttc tgggtcatgc 720  
tggttttac aggagattta taaaggactt cacaaagggtt 760

<210> 107

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 107

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Val Tyr Pro  
1 5 10 15

Ile Ser Glu Ser Lys Trp Val Ser Pro Val Glx Cys Val Pro Lys Lys  
20 25 30

Arg Gly Met Pro Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
35 40 45

Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Cys Pro Val Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Asp Arg Leu Val Gly Gln Glu Tyr Tyr Cys Phe Leu Glu Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Ala Phe Lys Glx Leu Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Glx Met Met Ala Ile  
130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Phe Arg Glu Ser Phe Asp Arg Cys Leu Glu Asn Trp Asp Arg  
165 170 175

Val Leu Ala Arg Cys Glu Glu Thr Asn Leu Ile Leu Asn Trp Lys Lys  
180 185 190

Cys His Phe Leu Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 108

<211> 761

<212> DNA

<213> Solanum tuberosum

<400> 108

gtgcgtaaag aggtttcaa gctctggatg caggtattgt ctatccaatt tcagacagca 60  
agtgggtcag tccagttcag tgtgtgccta aaaagggagg catgacggtg atcactaatg 120  
aaaaaaaaatga gttgattcca accaggacag tgacaggatg gcgaatatgc atggattaca 180  
gaaaattaaa tgaagctacc agaaaggatc actaccgggt tccttttatt gatcagatgc 240  
tggacaggtt ggctggacaa gaatattatt gtttcttggta tggttattca ggatacaacc 300  
aaatagtgtat tgcaccagag gaccagggga aaactacatt cacttgcatt tatggacat 360  
atgtttccaa gagaatgtcg tttggctat gcaatgctcc atccatttc caaagatgca 420  
tgatggccat cttccatgt aagggttgaag attttatgga aatattcatg gatgacttct 480  
cagtatttgg ggagtctttt gacaggtgct tggagaattt agacagagtg ttggctagat 540  
gcgagggaaac taattttgtc ctaaaacttggg aaaaatgtca tttccttagt aaggaaggga 600  
ttgtgttggg tcataagggtg tcaaagagag ggctggaagt tgatcgtgcc agagtggaaa 660  
taatcaaaaaa gctacctccc ccaatttctg ttaaagggtt gcgaagttt ttgggtcatg 720  
ttagttctta cggaaaggattc ataaaggact tcaccaaggt t 761

<210> 109

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 109

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Lys Trp Val Ser Pro Val Gln Cys Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
           35                 40                 45  
  
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn  
           50                 55                 60  
  
 Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met  
       65                 70                 75                 80  
  
 Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr  
       85                 90                 95  
  
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Gly Lys Thr  
      100                 105                 110  
  
 Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Val Ser Lys Arg Met Ser Phe  
      115                 120                 125  
  
 Gly Leu Cys Asn Ala Pro Ser Ile Phe Gln Arg Cys Met Met Ala Ile  
      130                 135                 140  
  
 Phe His Asp Lys Val Glu Asp Phe Met Glu Ile Phe Met Asp Asp Phe  
      145                 150                 155                 160  
  
 Ser Val Phe Gly Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asp Arg  
      165                 170                 175  
  
 Val Leu Ala Arg Cys Glu Glu Thr Asn Phe Val Leu Asn Trp Glu Lys  
      180                 185                 190  
  
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser  
      195                 200                 205  
  
 Lys Arg Gly Leu Glu Val Asp Arg Ala Arg Val Glu Ile Ile Lys Lys  
      210                 215                 220  
  
 Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His  
      225                 230                 235                 240  
  
 Val Ser Phe Tyr Glu Arg Phe Ile Lys Asp Phe Thr Lys Val  
      245                 250

<210> 110  
 <211> 762  
 <212> DNA  
 <213> Solanum tuberosum

<400> 110  
gtgcgttaagg aggtcctcaa gctgtctgat gcaggaattt ttttacccat ttatgtata 60  
aagtggatca gcccgatcca ctgtgtgccg aaaaagggag gcatgacgat tattactaat 120  
aaaaagaagg agttgatttc agctagaacg gtgatagagt ggcacatatg aatggactat 180  
aggagactaa atgaggcaac tagaaaaggaa cactacccag ttcccttcat tgatcaaatg 240  
ttggacaggt ttattggca agagtattat tgtttcctag atggctattc agatataat 300  
caaattgtga ttgcgcata agataaagag aaaactacat ttacttctct atatggaca 360  
tatgccttca agagaatgtc gtttggccg tgcaatgctc caaccacatt ccaaagatgc 420  
atgacagcca ttttcatga tatggtaaaa tattttgtgg agatattcat ggatgaattc 480  
ttagtcttg gggagtctt tgacacgtgt ctagaatatt tggacaatgt gcttgcaga 540  
tgtgaggaaa ctaatcccgt cctcaactgg gaaaaatgtc attttcttagt gaagaagggg 600  
attgtactag gccacaaggt ttcagaggaa ggactggaag ttgatcgtgg aaaagttagag 660  
gtaatttaaa agctaccccc tcaagtctc gttaaagggg tgagaaggaa ctttggcat 720  
tcttagttcg aaatgagatt cataaaagac ttcacaaaag tt 762

<210> 111  
<211> 254  
<212> PRT  
<213> Solanum tuberosum

<400> 111  
Val Arg Lys Glu Val Leu Lys Leu Ser Asp Ala Gly Ile Val Tyr Pro  
1 5 10 15  
  
Ile Tyr Asp Ile Lys Trp Ile Ser Pro Val His Cys Val Pro Lys Lys  
20 25 30  
  
Gly Gly Met Thr Ile Ile Thr Asn Glu Lys Lys Glu Leu Ile Ser Ala  
35 40 45  
  
Arg Thr Val Ile Glu Trp His Ile Glx Met Asp Tyr Arg Arg Leu Asn  
50 55 60  
  
Glu Ala Thr Arg Lys Glu His Tyr Pro Val Pro Phe Ile Asp Gln Met  
65 70 75 80  
  
Leu Asp Arg Phe Ile Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95  
  
Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glx Asp Lys Glu Lys Thr  
100 105 110  
  
Thr Phe Thr Ser Leu Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe  
115 120 125  
  
Gly Pro Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Thr Ala Ile

130	135	140
Phe His Asp Met Val Lys Tyr Phe Val Glu Ile Phe Met Asp Glu Phe		
145	150	155
		160
Leu Val Phe Gly Glu Ser Phe Asp Thr Cys Leu Glu Tyr Leu Asp Asn		
165	170	175
Val Leu Ala Arg Cys Glu Glu Thr Asn Pro Val Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Leu Val Lys Lys Gly Ile Val Leu Gly His Lys Val Ser		
195	200	205
Glu Glu Gly Leu Glu Val Asp Arg Gly Lys Val Glu Val Ile Glx Lys		
210	215	220
Leu Pro Pro Gln Val Phe Val Lys Gly Val Arg Arg Phe Leu Gly His		
225	230	235
Ser Arg Phe Glu Met Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 112  
 <211> 762  
 <212> DNA  
 <213> Solanum tuberosum

<400> 112  
 gtgcggaagg aggttttaa gctgctggat gcgggtattt tataccagat ttcagatagc 60  
 aaagggttct acccgattt aaaaaatgca gcatgacagt gatcaccaat 120  
 gaaaagaatg agctgattcc aaccaggaca gtgacagggt ggcgaatatg catggattat 180  
 atgaagttga atgaggccac cagaaaggat cactacccga ttcatttat tgatcagatg 240  
 ttggacaagt tagctgagta aaaatattat tggcttctgg ctgttattc aagataacaac 300  
 caatttctca ttgcaccaca ggaccaggag gaaactacat tcacttgtcc ttatggaca 360  
 tatgcttca agcgaatgtc gtttggctt tgcaatgctc caaccacctt ccaaagatgc 420  
 ataagggtcta tcttcatga tatgggtgaa gattttgtgg agatattcat ggatgacttc 480  
 tcagtctttt ggttagtctt tgagaggtgt ctggaaaatt ttgacagggt gctggctgtt 540  
 tgcgaggaaa ctaattttt cctaaactgg gaaaaatgtc attttcttagt gaaggaagg 600  
 attgtattgg gacataaggt gtcaaagtga aggcttgaag ttgatcgtgc caaagtggaa 660  
 gtcgttggaa acctaccttc cccattctt gttaaagggg tgagaagttt ttgggtcat 720  
 gctggttct ataggagatt tatcaaagac ttcactaagg tt 762

<210> 113  
 <211> 254  
 <212> PRT

<213> Solanum tuberosum

<400> 113

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Gln  
1 5 10 15

Ile Ser Asp Ser Lys Gly Val Tyr Pro Ile Glx Phe Val Pro Lys Lys  
20 25 30

Cys Ser Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
35 40 45

Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Met Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Tyr Pro Ile His Phe Ile Asp Gln Met  
65 70 75 80

Leu Asp Lys Leu Ala Glu Glx Lys Tyr Tyr Cys Phe Leu Ala Cys Tyr  
85 90 95

Ser Arg Tyr Asn Gln Phe Leu Ile Ala Pro Gln Asp Gln Glu Glu Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Ile Arg Ala Ile  
130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Phe Gly Glx Ser Phe Glu Arg Cys Leu Glu Asn Phe Asp Arg  
165 170 175

Val Leu Ala Val Cys Glu Glu Thr Asn Phe Phe Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Lys Glx Arg Leu Glu Val Asp Arg Ala Lys Val Glu Val Val Glu Asn  
210 215 220

Leu Pro Ser Pro Phe Ser Val Lys Gly Val Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 114  
<211> 793  
<212> DNA  
<213> Solanum tuberosum

<400> 114  
aacttttgc aagtcttaa tgaaggatgt tgctcagagaa gaagtcataca agtggctgga 60  
tacagggatt gtgtacccaa tatctgacaa taaatggca agtccagtgc agtgtgtgcc 120  
taaaaaggaa ggaatgacag ttgtgaccaa tgagaaaaat gagttgatcc ccacaagaac 180  
agtaactggg tggaggctat gcatggacta cagaaaaactc aatgaagcca ccaggaagga 240  
ccactattcg gtaccgttca ttgatcaa at gtagacagg ttggctggcc aagagtatta 300  
ctgtttcctt gatggttatt caaggtataa ttagatcgatc attgcacctg aggtcaaga 360  
gaatacgcaca ttcacttgcc catatggcac gtatgcattc aaacgcttgc cattcggctt 420  
gtgcaatgcc ccaaccctat ttcagagatg tatgatggca atcttccatg atatggtgg 480  
agattttgg aaagtataca tggacgattt ctccggttt ggtgagtcgt tcgaactttg 540  
tttatcta at cgtgatagag ttcttactag gtgtgaggag accaatttgg tgctgaactg 600  
ggagaagtgt cacttctgg tcagagaagg aattatgtt gggcagaaga tctccaaaag 660  
tgggctagaa gtagacaagg cgaagggttga agtgatttgg aagttgccac caccaatata 720  
agtaaaggaa gtgcgaagct tccttggaca tgctggttt tacaagaggt tcataaaggaa 780  
cttttcaaaag gtt 793

<210> 115  
<211> 264  
<212> PRT  
<213> Solanum tuberosum

<400> 115  
Thr Phe Val Lys Ser Leu Met Lys Asp Val Val Arg Glu Glu Val Ile  
1 5 10 15

Lys Trp Leu Asp Thr Gly Ile Val Tyr Pro Ile Ser Asp Asn Lys Trp  
20 25 30

Ala Ser Pro Val Gln Cys Val Pro Lys Lys Gly Gly Met Thr Val Val  
35 40 45

Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr Arg Thr Val Thr Gly Trp  
50 55 60

Arg Leu Cys Met Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp  
65 70 75 80

His Tyr Ser Val Pro Phe Ile Asp Gln Met Leu Asp Arg Leu Ala Gly

85	90	95
Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Arg Tyr Asn Glx Ile		
100	105	110
Val Ile Ala Pro Glu Asp Gln Glu Asn Thr Thr Phe Thr Cys Pro Tyr		
115	120	125
Gly Thr Tyr Ala Phe Lys Arg Leu Pro Phe Gly Leu Cys Asn Ala Pro		
130	135	140
Thr Leu Phe Gln Arg Cys Met Met Ala Ile Phe His Asp Met Val Glu		
145	150	155
Asp Phe Val Lys Val Tyr Met Asp Asp Phe Ser Val Phe Gly Glu Ser		
165	170	175
Phe Glu Leu Cys Leu Ser Asn Arg Asp Arg Val Leu Thr Arg Cys Glu		
180	185	190
Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Leu Val Arg		
195	200	205
Glu Gly Ile Met Leu Gly Gln Lys Ile Ser Lys Ser Gly Leu Glu Val		
210	215	220
Asp Lys Ala Lys Val Glu Val Ile Glu Lys Leu Pro Pro Pro Ile Glx		
225	230	235
Val Lys Gly Val Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Arg		
245	250	255
Phe Ile Lys Asp Phe Ser Lys Val		
260		

<210> 116  
 <211> 761  
 <212> DNA  
 <213> Platanus occidentalis

<400> 116  
 gtgcgttaagg aggtttcaa acttctaaa gtttgagtga tttatcctat ttaggatagg 60  
 aattgggtca gcccggttca agtggttcct aaaaagattg gaataaccgt tgtaaaaat 120  
 tagaatgatg agttgggtcc taccagtgtt cagaatgggt ggaggggtgt atagattata 180  
 gaaaattgaa tggtaacc cgcaaggatc acttcccttt accttttatt gatcaaatgc 240  
 ttgaaagggtt agttgggtcat tcctactatt gttcctaga tggttattca agttatttcc 300  
 agattgtaat tactccagag gattaagaaa agacaacttt tacatgtcca tttgggactt 360

ttgcatacg ttgcatgccc tttggccctt gcaatgcccc aaccacttc caaagggtga 420  
tggtagcat atttcatat tacattgaga atatcataga agttttatg gatgattca 480  
tagttatgg agactcctt aataatttc tgcataacct tacactgtt cttcaaagat 540  
gcatagaaac taaccttgtg ttaaattatg aaaaatgtca ttttatggtt gaacaaggta 600  
tagtttggg tcatgttatt tcatactaaag gaattgaggt agataaagct aaagttgata 660  
ttattcaatc ttaccttat ctcattagta tgccgaaagt tcattcttt ctggacatg 720  
caggttctta ccgaagattc attaaagact ttacaaaggt t 761

<210> 117

<211> 254

<212> PRT

<213> Platanus occidentalis

<400> 117

Val Arg Lys Glu Val Phe Lys Leu Leu Lys Val Glx Val Ile Tyr Pro  
1 5 10 15

Ile Glx Asp Arg Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Ile Gly Ile Thr Val Val Lys Asn Glx Asn Asp Glu Leu Val Pro Thr  
35 40 45

Ser Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Val Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Val Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Ser Tyr Phe Gln Ile Val Ile Thr Pro Glu Asp Glx Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Val Ser Ile  
130 135 140

Phe Ser Tyr Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ile Val Tyr Gly Asp Ser Phe Asn Asn Phe Leu His Asn Leu Thr Leu  
165 170 175

Val Leu Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Tyr Glu Lys  
180 185 190

Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Ile Ser  
195 200 205

Ser Lys Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ile Ile Gln Ser  
210 215 220

Leu Pro Tyr Leu Ile Ser Met Arg Lys Val His Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 118

<211> 762

<212> DNA

<213> Platanus occidentalis

<400> 118

gtgcgttaagg aagtttcaa gcttcttcaa gttggagtga tttatcttat ttcaataggc 60  
aattgggta gcccagttca agtggctcct aaaaagactg gaataaccgt tggaaaaat 120  
cagaatgtg agtttgttcc tacccatgtt cagaatgggt ggtgggttg tataaattat 180  
agaaaaattaa atgttataac ctgcaaggat cacttccctt tacctttat tgataaaatg 240  
cttggaaagg tagctggta ttcttactat tgtttccttg atggttatggg 300  
caaattgcaa ttacttcgga ggttcaagaa aagatgattt ttaagtgcctt attcgggact 360  
tttgcataatc gtcacatgcc ctttggcctt tgcaatgcctt caaccacttt ctaaagggtgt 420  
atggtttagca tattttcaga ttacatttgg aatatcatag aagtctttat ggatgatttc 480  
acagtttatg gagactccctt tgataattgtt ctgcataacc ttacacttgtt tattcaaaaga 540  
tgcataagaaa ctaaccttagt gttaaattct taaaaatgtc attttatgggt tgaacaagg 600  
atagttttgg gtcatgttgtt ttcatctagg ggaatttgggg tagataaaacc taaagttgtat 660  
attattcaaa cttaaccta ttccacttagt gtgcgagaag ttcggttctt tcttggacat 720  
gttagttttt actgaagatt cataaaagac ttccacaaagg tt 762

<210> 119

<211> 254

<212> PRT

<213> Platanus occidentalis

<400> 119

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Val Gly Val Ile Tyr Leu  
1 5 10 15

Ile Ser Asn Ser Asn Trp Val Ser Pro Val Gln Val Ala Pro Lys Lys  
20 25 30

Thr	Gly	Ile	Thr	Val	Val	Lys	Asn	Gln	Asn	Asp	Glu	Leu	Val	Pro	Thr
35														45	
His Val Gln Asn Gly Trp Trp Val Cys Ile Asn Tyr Arg Lys Leu Asn															
50				55								60			
Val	Ile	Thr	Cys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Lys	Met
65												75		80	
Leu	Glu	Arg	Leu	Ala	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
							85					90		95	
Leu	Gly	Tyr	Phe	Gln	Ile	Ala	Ile	Thr	Ser	Glu	Asp	Gln	Glu	Lys	Met
							100					105		110	
Ile	Phe	Lys	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	His	Met	Pro	Phe
							115					120		125	
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Glx	Arg	Cys	Met	Val	Ser	Ile
							130					135		140	
Phe	Ser	Asp	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145								150				155		160	
Thr	Val	Tyr	Gly	Asp	Ser	Phe	Asp	Asn	Cys	Leu	His	Asn	Leu	Thr	Leu
													165	170	175
Val	Ile	Gln	Arg	Cys	Ile	Glu	Thr	Asn	Leu	Val	Leu	Asn	Ser	Glx	Lys
												180	185	190	
Cys	His	Phe	Met	Val	Glu	Gln	Gly	Ile	Val	Leu	Gly	His	Val	Val	Ser
								195				200		205	
Ser	Arg	Gly	Ile	Glu	Val	Asp	Lys	Pro	Lys	Val	Asp	Ile	Ile	Gln	Thr
								210			215		220		
Leu	Pro	Tyr	Ser	Thr	Ser	Val	Arg	Glu	Val	Arg	Ser	Phe	Leu	Gly	His
								225			230		235		240
Val	Gly	Phe	Tyr	Glx	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
								245			250				

<210> 120  
<211> 759  
<212> DNA  
<213> Platanus occidentalis

<400> 120

gtgcggaaag aggttttaa gctttggat gtagggatta tatacccaat tttttagt 60  
aattaggtaa gtcccactca agtggaccca agaattctgg tgtgactgta gtaaaaatg 120  
caaatgatga attgattcca aatagactca ctattggtt gcgtgtatgc attaactata 180  
agaagttgaa ctcagtact aggaaggacc attccctt accattcatg actaaatcct 240  
agaaagggtt gctggtcaca aattttatta tttcctatat gtttattcta gatataacta 300  
aatagagatt gcacctgagg actaagaaaa taccacttt acatgtccat ttggacttt 360  
tgcttatcga aggatgtcat ttggattatg taatgctttt gccacgttct aaagatgtcat 420  
gtttagtata ttttagtata tggtagaaca tttcttgag gtgttatgg atttttttg 480  
tttttgtaa ttcatttgc gattgttgc ataatttcaa aaaagtgtt aatagatgtg 540  
aaggaaaaaa acatcattt gaattgagag aagtgtcatt tcattgtc taaaagaatt 600  
gtacttggtc acattgtc tcccaagga attaaagtgg tcaaagccaa aattgaattt 660  
atagtcaatt tgcctagccc aaagactttt aaagacattc gatctttt aggtcatgca 720  
ggatttaaca aaaggttcat caaagacttc acgaaagtt 759

<210> 121

<211> 254

<212> PRT

<213> Platanus occidentalis

<400> 121

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro  
1 5 10 15

Ile Phe Tyr Ser Asn Glx Val Ser Pro Thr Gln Val Val Pro Lys Asn  
20 25 30

Ser Gly Val Thr Val Val Lys Asn Ala Asn Asp Glu Leu Ile Pro Asn  
35 40 45

Arg Leu Thr Ile Gly Trp Arg Val Cys Ile Asn Tyr Lys Lys Leu Asn  
50 55 60

Ser Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Glx Ile  
65 70 75 80

Leu Glu Arg Val Ala Gly His Lys Phe Tyr Tyr Phe Leu Tyr Gly Tyr  
85 90 95

Ser Arg Tyr Asn Glx Ile Glu Ile Ala Pro Glu Asp Glx Glu Asn Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Leu Ala Thr Phe Glx Arg Cys Met Leu Ser Ile

130

135

140

Phe Ser Asp Met Val Glu His Phe Leu Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Phe Val Phe Gly Asn Ser Phe Asp Asp Cys Leu His Asn Leu Lys Lys  
165 170 175

Val Leu Asn Arg Cys Glu Glu Lys Asn Ile Ile Leu Asn Glx Glu Lys  
180 185 190

Cys His Phe Met Val Ser Lys Arg Ile Val Leu Gly His Ile Val Ser  
195 200 205

Ser Gln Gly Ile Lys Val Val Lys Ala Lys Ile Glu Leu Ile Val Asn  
210 215 220

Leu Pro Ser Pro Lys Thr Leu Lys Asp Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Asn Lys Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 122

<211> 761

<212> DNA

<213> Platanus occidentalis

<400> 122

tgcgtaaaga ggtggtaaag cttcttgaag ttggagtgtat ttatcctatt tcggatagca 60  
attgggttag cccggttcaa gtgggtccta aaaagactgg aataaccgtt gtaaaaatc 120  
aaaatgatga gttagttcct acccgtgttc agaatgggtg gcagggttgt atagattata 180  
taaaattaaa tggtaacc cgcaaggatc acttccctt acctttatt gatcaaatgt 240  
ttgaaagggtt agctggcat tcttactatt gttccttga tggatattca tggatattttt 300  
agattgcaat tactccagag gatcaagaaa agacgacttt tacgtgccca ttcggactt 360  
tttcatatcg ttgcatgccccc tttggccccc gcaacgcccc agccactttc caaagggtgt 420  
tggtagcat atttcagat tacattgaga atatcataga agtctttatg gatgattca 480  
tagtttatga agactccccc gataattgtc tgcatcaccc tacacttggtt tttaaagat 540  
gcatagaaac taaccttgc taaaatttg aaaaatgtca tggtatgggtt gaataaggta 600  
tagttttggg tcatgttgc tcatctatgg gaattgaggt agataaaagtt aaagttgata 660  
ttattcaatc tttacccat cccatttagtgc tgcatggaaatg tcgttctttt ctggacatg 720  
cgggtttta ccaaagattc attaaagact tcacgaaagt t 761

<210> 123

<211> 253

<212> PRT

<213> Platanus occidentalis

<400> 123

Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Glu	Val	Gly	Val	Ile	Tyr	Pro	Ile
1			5					10						15	
Ser	Asp	Ser	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys	Thr
				20				25					30		
Gly	Ile	Thr	Val	Val	Lys	Asn	Gln	Asn	Asp	Glu	Leu	Val	Pro	Thr	Arg
				35				40					45		
Val	Gln	Asn	Gly	Trp	Gln	Val	Cys	Ile	Asp	Tyr	Ile	Lys	Leu	Asn	Val
					50		55				60				
Val	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	Phe
				65		70				75			80		
Glu	Arg	Leu	Ala	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser
				85				90					95		
Cys	Tyr	Phe	Glx	Ile	Ala	Ile	Thr	Pro	Glu	Asp	Gln	Glu	Lys	Thr	Thr
				100				105				110			
Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ser	Tyr	Arg	Cys	Met	Pro	Phe	Gly
				115				120			125				
Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Val	Ser	Ile	Phe
				130				135			140				
Ser	Asp	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Ile
				145				150			155		160		
Val	Tyr	Glu	Asp	Ser	Phe	Asp	Asn	Cys	Leu	His	Asn	Leu	Thr	Leu	Val
				165				170			175				
Phe	Glx	Arg	Cys	Ile	Glu	Thr	Asn	Leu	Val	Leu	Asn	Phe	Glu	Lys	Cys
				180				185			190				
His	Val	Met	Val	Glu	Glx	Gly	Ile	Val	Leu	Gly	His	Val	Val	Ser	Ser
				195				200			205				
Met	Gly	Ile	Glu	Val	Asp	Lys	Val	Lys	Val	Asp	Ile	Ile	Gln	Ser	Leu
				210				215			220				
Pro	Tyr	Pro	Ile	Ser	Val	Gln	Glu	Val	Arg	Ser	Phe	Leu	Gly	His	Ala
				225				230			235		240		

Gly Phe Tyr Gln Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 124  
<211> 761  
<212> DNA  
<213> Sorghum bicolor

<400> 124  
gtgcgtaaag aggtcttcaa gctctatcat gctgggatta tttatcctgt gccgcatagt 60  
gagtgggtta gccctgttca agtagtgcca aagaaggag gaatgacggt cgtaggaat 120  
gagaagaatg aactcatccc tcaacgaatt gtcaactgggt ggcgtatgtg tattgactat 180  
caaaaactca acacggctac aaagaaaagat aaccttccgt tacccttcat tgatgaaaatg 240  
ttggaacggc ttgcaaacc a cttttcttc tttttcttg atggttattc tgatgatcac 300  
caaattccaa tccacccaga tgaccaagaa aagactacct ttacatgccc gtatgaaact 360  
tatgcataac gacgaatgtc gttcggactg tgcaatgctc cagttcttt ccaacggtgc 420  
atgatgtcta ttttctcgga catgatttag aagatcatgg aggtttcat ggatgatttt 480  
accgtctatg gtaaaacctt cgatcattgt ttggagaatt tagatagagt ctgcagcga 540  
tgtgaagaaa agcacttaat cctgaactgg gaaaaatgcc attttatggt tcaggaagga 600  
atagtgttag gacataaaagt gtccgaacgt ggtatagagg tggacaaagc aaagattgaa 660  
gttattgaaa aacttccacc tccccacgaat gtgaaaggat ccgtagctc ttgggacatg 720  
cagggttcta tagatgctc ataaaagact tcacaaaggt t 761

<210> 125  
<211> 254  
<212> PRT  
<213> Sorghum bicolor

<400> 125  
Val Arg Lys Glu Val Phe Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln  
35 40 45

Arg Ile Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn  
50 55 60

Thr Ala Thr Lys Lys Asp Asn Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Glx Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Thr Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Cys Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 126

<211> 762

<212> DNA

<213> Sorghum bicolor

<400> 126

gtgcggaaagg aggtccttaa attgctgcat gcagggatta tatatcctgt gccgcacagt 60  
gagtgggtga gcccagtaca agttgtgcct aaaaaaggag gcatgactgt tattataaat 120  
aaaaagaacg agctaattcc gcaacgcacc gtcacaggat ggcagatgtg catagactat 180  
aaaaaactaa acaaagccac gagaaaggat cacttcctt tacctttat agatgagatg 240  
ctagagcggt tagcaaaccac ttctgttttc tgtttcttag atggatattc agggtatcat 300  
cagatcccga tccatcccga tgatcaaagc aaaaccactt ttacatgccc ttatgaaact 360  
tatgcttacc gtagaatgtc ttttgggta tgtaatgcac cagttcttt tcaaagatgc 420  
atgatgtcta tattttctga tatgattgaa gagattatgg aagttttcat ggatgatttc 480  
tctgtttatg gaaaagctt tgatagttgt cttgaaaaact tagacaaggt ttgcaaagt 540  
tgtgaagaaa agcacttaat ccttaattgg gaaaatgtc attttatggt taggaaagga 600

atagtgctag gacacttagt gtctgaaagg ggtattgagg tagacaaagc taaaattgaa 660  
gtaattgaac aactacctcc acctgtaat ataaaaggaa ttcaagctt tcttggccat 720.  
gctggtttt atcgttagatt catcaaagat ttcacgaaag tt 762

<210> 127  
<211> 254  
<212> PRT  
<213> Sorghum bicolor

<400> 127

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Ala	Gly	Ile	Ile	Tyr	Pro
1				5				10						15	

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile Ile Asn Glu Lys Asn Glu Leu Ile Pro Gln  
35 40 45

Arg Thr Val Thr Gly Trp Gln Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Glu Ile Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Lys Ala Phe Asp Ser Cys Leu Glu Asn Leu Asp Lys  
165 170 175

Val Leu Gln Ser Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser

195

200

205

Glu Arg Gly Ile Glu Val Asp Lys Ala Glu Ile Glu Val Ile Glu Gln  
210 215 220

Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 128

<211> 762

<212> DNA

<213> Sorghum bicolor

<400> 128

gtgcggaagg aagtcttaaa gctttacac actaggatta tttatctcggt tcctcatagt 60  
gagtgggtta gcacggtaca agttgtgccca aagaaaggag gaatgtcggt tgtaggaat 120  
gagaagaacg aattcatccc tcaacaaact gtcactgggt ggcgtatgtc cattgactac 180  
caaaaaactca acaaggccac aaggaaagat cactcccggt tacctttcat tgatgaaatg 240  
ttgtaatggc ttacaaatca ctcgttctt tgttccttg aagggtattc cagatatcat 300  
caaattccga tccaccacga tgaccaaagt aagactactt tcacatgacc ctatgaaact 360  
tacgcataacc gacgaatgtc gttcaggta tgtaatgctc cagcttctt tcaacgggtgc 420  
atgatgtcta tttttccaa tatgatttag aaaaatcatgg aggtattcac ggatgatgtt 480  
accgtatatg gcaaaacctt tgatgattgt ttagagaatt tggacaaagt cttacaattg 540  
tgtgaaggaa agcacttaat cgtaaactag gagaatgcc attttatggc ccgagaagga 600  
atagtgttag ggcacaaggt gtccgaacgt gggatagagg tggatagagc caagattgaa 660  
gttattgaaa aacttccacc tcccacaaat gtgaaagaca tccgcagttt tcttggacat 720  
gcagggttct ataggcgctt catcaaagat ttccaccaagg tt 762

<210> 129

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 129

Val Arg Lys Glu Val Leu Lys Leu Leu His Thr Arg Ile Ile Tyr Leu  
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Thr Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Ser Val Val Arg Asn Glu Lys Asn Glu Phe Ile Pro Gln  
35 40 45

<210> 130  
<211> 761  
<212> DNA  
<213> Sorghum bicolor

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<400> 130  
gtgcgttaagg aggttttaa gctgctgcat gcagagatta tataatcatgt gccgcacagt 60  
qaqtqqqtaaa qcccaqttca aqttatqcct aaaaqqqqaq qcatgattqt tgttacqaat 120
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gaaaagaacg agctaattcc gcaacgcacc gtcacagggt ggccggatgtg catagactat 180  
agaaaaactaa acaaagccac gagaaaggat cattttcctt tacctttcat agatgagatg 240  
ctagagcgat tagcaaaccat ttcgttcttc tgtttcttag atggataatt agggtatcac 300  
cagatcccaa tcaatcttga tgatcaaagc aaaaccactt ttccatgccc acatggaact 360  
tatgcttacc gtagaatgtc ttttgggta tgtaatgcac cagcttctt tcaaagatgc 420  
atgatgtctg tattttctaa tatgattgaa gagattatgg aattttcatg gatgatttct 480  
ctgttatgg aaaaactttt gatagttgtc ttgaaaactt agacagggtt ttgcaaagat 540  
gtgaagaaaa gtacttagtc cttaatttga aaaaatgtca ttttatggtt agggaaaggaa 600  
tagtgctggg acacccatgtc tctgaaagag gtattgaggt cgacaaagct aaaaattgaag 660  
taattgaaca actaccccca cctttgaata taaaaggaat tcgaagctt cttggccatg 720  
ctggtttta tcgttagattc attaaggact ttacaaaggt t 761

<210> 131

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 131

Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Glu Ile Ile Tyr His  
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Ile Val Val Thr Asn Glu Lys Asn Glu Leu Ile Pro Gln  
35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Glx  
85 90 95

Leu Gly Tyr His Gln Ile Pro Ile Asn Leu Asp Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Pro Cys Pro His Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Val  
130 135 140

Phe Ser Asn Met Ile Glu Glu Ile Met Glu Ile Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Lys Thr Phe Asp Ser Cys Leu Glu Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Lys Tyr Leu Val Leu Asn Trp Lys Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln  
210 215 220

Leu Pro Pro Pro Leu Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 132

<211> 763

<212> DNA

<213> Sorghum bicolor

<400> 132

gtgcggaaag aggtcgtcaa gctctatcat gctgggatta tttatccgt gccacatagt 60  
gagtgggtta gccctgttca agtagtgcca aagaaaagaag gaatgacggt cgtaggaat 120  
gagaagaatg aactcatccc tcaacaatt gtcactagat ggcgtatgtg tattgactat 180  
cgaaaaactca acaaagctac aaagaaaagat cactttccgt tacccttcat tgatgaaatg 240  
ttggaatggc ttgcaaaccac ctctttcttc tgtttccttg atggttattc tggatatcac 300  
caaatcccaa tccacccaga tgaccaagaa aagactacct ttacatgccc gtattgaact 360  
tatgcatact gacgaatgtc gttcggattt tgcaatgctc tagcttcttt tccagcggtg 420  
catgatgtct attttctcgg acatgattga gaagatcatg gaggtttca tggatgattt 480  
taccgtctat ggcaaaacct tcgatcattt tttggagaat ttagatagag tcttgcagcg 540  
atgtgaggaa aatcaactaa tcttgaactg ggagaaatgt cattttatgg ttcaggaagg 600  
aatagtgcata ggacataaag tgtccgaacg tggatagat gtggacaaag caaagattaa 660  
agtttattgaa aaacttccac ctcacacagaa tgtgaaagga atccatagct ttttgggaca 720  
tgcagggttc tataagacgct tcatcaagga tttcacaaag gtt 763

<210> 133

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 133

Val Arg Lys Glu Val Val Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro

1

5

10

15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Glu Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln  
35 40 45

Gln Ile Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Glx Thr Tyr Ala Tyr Glx Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Asn His Leu Ile Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Glu Arg Gly Ile Asp Val Asp Lys Ala Lys Ile Lys Val Ile Glu Lys  
210 215 220

Leu Pro Pro His Thr Asn Val Lys Gly Ile His Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 134  
<211> 756  
<212> DNA  
<213> Sorghum bicolor

<400> 134  
aaggagggtt tcaagttgct gcatgcaggg attatatatc ttgtgccgca tagtgagtgg 60  
gtaagcccag ttcaagttgt gcctaaaaag ggaggcatga ctattattat gaatgaaaag 120  
aacgagctaa ttccgcaacg caccgttaca gtatggcgga tgtgcataga ctatagaaaa 180  
ctaaacaaag ccacgagaga ghatcacattt ccttacatt tcatacatga gatgcttagag 240  
tggtagcaa accattcggtt cttctgttcc ttagatggat attgagggtt tcatcagatc 300  
ccgatccatc ccgatgatca aagcaaaacc actttacat gcccataatgg aacttatgct 360  
taccgttagaa tgtctttgg gttatgtaat gcactagctt ctttcaaag atgcatgatg 420  
tctatatttt ctgatatgtat tgaagagatt atgaaagttt tcatggatga tttctctgtt 480  
tatggaaaaa ctttgatag ttgtcttaaa aacttagaca aggtttgca aagatgtgaa 540  
gaaaagcaact tagtccttaa ttggggaaaaa tgtcattca tggtaggga aggaatagtg 600  
ctgggacact tagtgtctga aagagctatt gaggtagata aagctaaaat tgaagtaatt 660  
gaacaactac gtccacctgtt gaacataaaa ggaatttgaa gctttcttgg ccatgctggt 720  
tttcatcgta gattcataaaa agactttaca aagttt 756

<210> 135  
<211> 252  
<212> PRT  
<213> Sorghum bicolor

<400> 135  
Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Leu Val Pro  
1 5 10 15  
  
His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly  
20 25 30  
  
Met Thr Ile Ile Met Asn Glu Asn Glu Leu Ile Pro Gln Arg Thr  
35 40 45  
  
Val Thr Val Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn Lys Ala  
50 55 60  
  
Thr Arg Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met Leu Glu  
65 70 75 80  
  
Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr Glx Gly  
85 90 95  
  
Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Ser Lys Thr Thr Phe  
100 105 110

Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe	Gly	Leu
		115					120							125	
Cys	Asn	Ala	Leu	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile	Phe	Ser
		130					135							140	
Asp	Met	Ile	Glu	Glu	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val
		145				150				155				160	
Tyr	Gly	Lys	Thr	Phe	Asp	Ser	Cys	Leu	Lys	Asn	Leu	Asp	Lys	Val	Leu
		165						170						175	
Gln	Arg	Cys	Glu	Glu	Lys	His	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His
		180					185						190		
Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Leu	Val	Ser	Glu	Arg
		195					200						205		
Ala	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Glu	Gln	Leu	Arg
		210				215					220				
Pro	Pro	Val	Asn	Ile	Lys	Gly	Ile	Glx	Ser	Phe	Leu	Gly	His	Ala	Gly
		225					230			235				240	
Phe	His	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val				
		245						250							

<210> 136  
<211> 762  
<212> DNA  
<213> Glycine max

<400> 136  
gtgcgttaagg aggttgtcaa gctttggag gttgggctca tataacctcat ctctgacagc 60  
gcttggtaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaaat 120  
gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180  
tgcaagttga atgaagccac acggaaggac cattccccct tacctttcat ggatcagatg 240  
ctggagagggc ttgcaggggca ggcatactac tgtttcttgg atagatattc aggataacaac 300  
caaatcgccgg tagaccccg agatcaggag aagatggcct ttacatgccc cttggcgtc 360  
tttgcttaca gaaggatgtc attcaggatgtt tgtaacgcac cagccacatt tcagagggtgc 420  
gtgctggcca tttttcaga catggtgag aagagcatcg aggtatttat ggatgaattc 480  
tcgatttttgc accccttatt tgacagtgc ttaaggaact tagagatggt actacagagg 540  
tgcgtataga ctaacttggt actaaattag gaaaaatgtc atttcatgggt tcgagaggga 600  
atagtgtatgg accacaatat ctcagctaga gggattgagg ttgatcaggc aaagatagac 660  
gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt ctttagggcat 720  
gcaggttct acaggaggtt tatcaaggac ttcaccaagg tt 762

<210> 137  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 137

Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu  
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys  
20 25 30

Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr  
35 40 45

Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met  
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile  
130 135 140

Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe  
145 150 155 160

Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met  
165 170 175

Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Met Asp His Asn Ile Ser  
195 200 205

Ala Arg Gly Ile Glu Val Asp Gln Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 138  
<211> 763  
<212> DNA  
<213> Glycine max

<400> 138  
gtgcgttaagg aggtctttaa gttcttgag gctgggctca tatatcccat ctctaatacg 60  
acttaggtaa gcccagtaca ggtggttccc aagaaaagggtg gaatgacagt agtacagaat 120  
gagaagaatg acttgatacc aacacgaact gtcactagct ggccaatatg catcgattat 180  
cgcaagctga atgaggccac ccggaaaggac cacttccctc taccttctat ggatcagatg 240  
ttggagagac ttgcagggca ggcgtattat tgtttcttgg atggatactc gagatataat 300  
cagattgcgg tggaccctag agaccaagag aagacgacat tcacatgcc ttttggcgt 360  
ctttgcttac agaaggatgc cattcgggtt atgtaatgca ccagccacat ttcagaggtg 420  
catgctggcc attttttcag acatggtgg aaaaaatatc gaggtattca tggatgactt 480  
ttcagttttt gggccctcat ttgacagttt tttgaggaac ctagagatgg tacttttagag 540  
gtgcgttagag actaatttag tgctgaactg ggagaagtgt catttatgg ttcgagaggg 600  
catagtcctg agccacaaga tctcagctag aggatttag gttgaccggg caaagataga 660  
cgtcatagag aagctgccac caccattgaa tattaaagggt gtcagaagtt tcttagggca 720  
tgcaggattc tacaggagat tcataaaagga ctttacaaag gtt 763

<210> 139  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 139  
Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asn Ser Thr Glx Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Gln Asn Glu Lys Asn Asp Leu Ile Pro Thr  
35 40 45

Arg Thr Val Thr Ser Trp Arg Ile Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met

65

70

75

80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95

Ser Arg Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Thr  
 100 105 110

Thr Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile  
 130 135 140

Phe Ser Asp Met Val Glu Lys Asn Ile Glu Val Phe Met Asp Asp Phe  
 145 150 155 160

Ser Val Phe Gly Pro Ser Phe Asp Ser Cys Leu Arg Asn Leu Glu Met  
 165 170 175

Val Leu Glx Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Lys Ile Ser  
 195 200 205

Ala Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220

Leu Pro Pro Pro Leu Asn Ile Lys Gly Val Arg Ser Phe Leu Gly His  
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

&lt;210&gt; 140

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;400&gt; 140

gtgcgcaagg aggtttgaa gcttctagag gttggctta tctacccat ctccgacagc 60  
 gcttggtaa gcccagtctt ggtggtgtcg aagaaagagg gcatgacagt cattcgaaat 120  
 gaaaagaatg acctgatacc aacacgaact gtcaacttagtt ggaaattatg catcgattac 180  
 cgcaagctca acgaagccac aaggaaagac cattccctc tacccttcat ggatcagatg 240  
 ttggagagac ttgcaggaca cgcttattat tgcttcttgg atgcatactt tggatataat 300  
 cagattgtg tagaccccaa ggatcaggag aagatggcct tcacatgccccc ttttgggtgtc 360

tttgcctata gacggattcc atttgggttg tgcaatgcac ctaccacatt ccaaatgtgc 420  
atgttggcca ttttgcaga tatagtggag aaaagcatcg aagtattcat ggatgacttt 480  
tcagtatttg tgccctcatt agaaagttgt ttgaagaagt tggagatggt actacaaaga 540  
tgcgtggaaa caaacttagt actaaattgg gagaagtgtc acttcatggt tcgagaaggc 600  
atagtcttag gccataaaaat ttgcaccga ggaattgagg tagaccaaacc aaagattgat 660  
gtcattgaaa agttgccacc accatcaaattt gttaaaggca tcaggagctt cctaggacaa 720  
gccaggttct acagaagatt catcaaggac ttcacaaaag tt 762

<210> 141  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 141  
Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro  
1 5 10 15  
  
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Leu Val Val Ser Lys Lys  
20 25 30  
  
Glu Gly Met Thr Val Ile Arg Asn Glu Lys Asn Asp Leu Ile Pro Thr  
35 40 45  
  
Arg Thr Val Thr Ser Trp Lys Leu Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60  
  
Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80  
  
Leu Glu Arg Leu Ala Gly His Ala Tyr Tyr Cys Phe Leu Asp Ala Tyr  
85 90 95  
  
Phe Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Met  
100 105 110  
  
Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Ile Pro Phe  
115 120 125  
  
Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Met Cys Met Leu Ala Ile  
130 135 140  
  
Phe Ala Asp Ile Val Glu Lys Ser Ile Glu Val Phe Met Asp Asp Phe  
145 150 155 160  
  
Ser Val Phe Val Pro Ser Leu Glu Ser Cys Leu Lys Lys Leu Glu Met  
165 170 175

Val Leu Gln Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Thr Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Ser Asn Val Lys Gly Ile Arg Ser Phe Leu Gly Gln  
225 230 235 240

Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 142

<211> 762

<212> DNA

<213> Glycine max

<400> 142

gtgcggaaagg aggttattaa gttgctagag gcagggctca tttaccta at ctcagatagt 60  
tcataggtta gtcctgttca tggtgctctg aaaaagggag gtatgacagt gataaagaat 120  
gatagagatg agttaattcc tacaagaata gttactggat ggaggatggg tattgattac 180  
aagaagctaa atgaagccac caggaaagac cattacccgc ttccccttcat ggatcaaatg 240  
cttgagagac ttgcagggca atcttcctac tatttattag atggatactc gggctacaat 300  
caaattgcag tggatcctca ggaccaagaa aagacagctt tcacatgtcc ttttgggtga 360  
tttgcttatac gccgcatgtc gttcggttta tgtaatgccc caactactt ccagagatgt 420  
atgatggcaa ttttgctga catggtaaag aaatgtattg aagttttat ggacgatttc 480  
tctgtcttg gtgcatttt tgaaaattgc ctagcaaatt tagagaaagt gttacaacgc 540  
tatgaagaat ctaatttgtt gctcaactgg gaaaaatgtc actttatggt tcaagaaggt 600  
atcatgctgg gacacaagat ttctagaaga ggaattaagg tggataaggc aaagattgag 660  
gttattgata aacttccacc tctagttat gtttagaggca tacgaagttt ttgggtcat 720  
gctagattct atcgatgatt tatcaaggac ttcaccaaaag tt 762

<210> 143

<211> 254

<212> PRT

<213> Glycine max

<400> 143

Val Arg Lys Glu Val Ile Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu  
1 5 10 15

Ile Ser Asp Ser Ser Glx Val Ser Pro Val His Val Ala Leu Lys Lys  
20 25 30

Gly	Gly	Met	Thr	Val	Ile	Lys	Asn	Asp	Arg	Asp	Glu	Leu	Ile	Pro	Thr
		35					40				45				
Arg	Ile	Val	Thr	Gly	Trp	Arg	Met	Gly	Ile	Asp	Tyr	Lys	Lys	Leu	Asn
		50				55				60					
Glu	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
		65				70			75			80			
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ser	Ser	Tyr	Tyr	Leu	Leu	Asp	Gly	Tyr
		85					90				95				
Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Gln	Asp	Gln	Glu	Lys	Thr
		100					105				110				
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120			125					
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
		130				135				140					
Phe	Ala	Asp	Met	Val	Lys	Lys	Cys	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
		145				150			155			160			
Ser	Val	Phe	Gly	Ala	Ser	Phe	Glu	Asn	Cys	Leu	Ala	Asn	Leu	Glu	Lys
		165					170				175				
Val	Leu	Gln	Arg	Tyr	Glu	Glu	Ser	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180				185				190					
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Ile	Ser
		195					200			205					
Arg	Arg	Gly	Ile	Lys	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Asp	Lys
		210				215				220					
Leu	Pro	Pro	Leu	Val	Asn	Val	Arg	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
		225				230			235			240			
Ala	Arg	Phe	Tyr	Arg	Glx	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
					245				250						

<210> 144

<211> 761

<212> DNA

<213> Glycine max

<400> 144

gtgcggaaagg aggtctttaa gttgctggaa gcaggcccta tttatcccat ttcggatagt 60  
gcatgggtta gccctatgca agttgtccct aagaaggag gtatgacagt cattaagaat 120  
gataaagatg agttgatatc cacaaggacc gtcaccgggt ggagaatgtg cattgactat 180  
cgaaaagctga atgatgcacc cggaaggacc attatccact cccttcatg gcccataatgc 240  
ttgaaagact tggtggcaa tcctattatt gtttctaga tggatattat ggttataatc 300  
agattgttgt agatccaaa gatcaagaga agacagctt cacctaccct tttggtgtat 360  
tcgcataatca gtgcattgcct tttggctat gcaatgcccc agctacattt cagaggtgta 420  
tgatggctat ttttctgtat atggtgaaa tatgcattga agtttcatg gacgatttct 480  
ctatTTTgg gccatcctt gaagggtgct tatcaaatct tgaaaaagta taaaagagat 540  
gtgaagagtc caatctagtt ctcaattgga agaaatgcca tttcatggtt caagaaggaa 600  
taatgttgg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgtat 660  
taattgagaa actacttgct cccatgaatg tcaaggaaat aagaagcttc tttaggacatg 720  
cagggttcta caggcgattc ataaaagact tcacccaaagt t 761

<210> 145

<211> 254

<212> PRT

<213> Glycine max

<400> 145

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Pro Met Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr  
35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Gly His Met  
65 70 75 80

Leu Glu Arg Leu Val Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Tyr Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr  
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Gln Cys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile

130

135

140

Phe Ser Asp Met Val Glu Ile Cys Ile Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Lys  
165 170 175

Val Leu Lys Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Lys Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser  
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Leu Ala Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 146

<211> 762

<212> DNA

<213> Glycine max

<400> 146

gtgcgttaagg aggtggtaaa gttgcttcaa gtaggactaa tttatccaa ctctgatagt 60  
gcttgggtga gttcgaacta ggtggtcct aagaaaggtg gtatgacggt gatccacaat 120  
gataagaatg atcttattcc tacacagaca atcattaggt ggcaaatgtg tattgactat 180  
cacaagttga atgatgtcac caagaaggac catttcctc tgccattcat ggaccaaatg 240  
ttagagaggt tagctggcca agcttttat tgtttttg aggttattc tgggtataac 300  
caaatacgcc tgcatttcaa agatcaagag aagactacta tcatacgccc atttgggtgc 360  
tttgcttaca gacaaatgtc atttgaactg tgtaatgccc ctaccacctt ctagagattc 420  
atgatggcca ttttgctga ccttggag aaatgcatacg aggtgttcat gaatgatttc 480  
tctatttcg gctttccctt ttatcattgt ttatccaaacc tggaatttagt gttacaacgg 540  
tgtgcggaaa ccaatttggt gatgaactgg gagaaatgtc atttcatggt ccaagagggg 600  
attgtcttag gccacaagat ctcttccaga gggttggaaag tggacaaggc aaaaattgat 660  
gttattgaga agttgcctcc acctatgaat gtgaaaggca tccgaagttt tctcgaatat 720  
gttggatttt ataggaggtt catcaaagac ttcacgaaag tt 762

<210> 147

<211> 254

<212> PRT

<213> Glycine max

<400> 147

Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Ser Asn Glx Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile His Asn Asp Lys Asn Asp Leu Ile Pro Thr  
35 40 45

Gln Thr Ile Ile Arg Trp Gln Met Cys Ile Asp Tyr His Lys Leu Asn  
50 55 60

Asp Val Thr Lys Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Phe Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val His Leu Lys Asp Gln Glu Lys Thr  
100 105 110

Thr Ile Ile Cys Pro Phe Gly Val Phe Ala Tyr Arg Gln Met Ser Phe  
115 120 125

Glu Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Phe Met Met Ala Ile  
130 135 140

Phe Ala Asp Leu Val Glu Lys Cys Ile Glu Val Phe Met Asn Asp Phe  
145 150 155 160

Ser Ile Phe Gly Ser Ser Phe Tyr His Cys Leu Ser Asn Leu Glu Leu  
165 170 175

Val Leu Gln Arg Cys Ala Glu Thr Asn Leu Leu Met Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Ser Arg Gly Leu Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Glu Tyr  
225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 148  
<211> 762  
<212> DNA  
<213> Glycine max

<400> 148  
gtgcgttaagg aggttctcaa gctttggag gttggctca tataacctat ctctgacagc 60  
gcttggtaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120  
gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180  
tgcaagttga atgaagccac acggaaggac cattccccct taccttcat ggatcagatg 240  
ctggagggc ttgcagggca ggcataactac tgtttcttgg atagatattc agataacaac 300  
caaatcgccg tagacccccag agatcaggag aagatggcct ttacatgccc cttggcgtc 360  
tttgcttaca gaaggatgtc attcaggta tgtaacgcac cagccacatt tcagaggtgc 420  
atgctggcca tttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480  
tcgatttttgc acccatttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540  
tgcgtataga ctaacttgtt actaaattag gaaaaatgtc atttcattgtt tcgagaggga 600  
atagtgtatgg gccacaatat ctcagctaga gggattgagg ttgatcagac aaagatagac 660  
gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt ctttagggcat 720  
gcaggtttct acaggaggtt cataaaagac ttcacaaaagg tt 762

<210> 149  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 149  
Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu  
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys  
20 25 30

Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr  
35 40 45

Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met  
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile  
130 135 140

Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe  
145 150 155 160

Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met  
165 170 175

Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Met Gly His Asn Ile Ser  
195 200 205

Ala Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 150

<211> 761

<212> DNA

<213> Glycine max

<400> 150

gtgcgtaagg aggtttttaa gttgctggaa gcaggtctta tttatcccat ttccggatagt 60  
gcatgggtta gccctgtgca gggtgtcccc aaaaaagaag gtaagacagt cattaaggat 120  
aaaaaggatg agttgatatac cacaaggact atcacccgggt ggagaatgtg cattgactat 180  
cagaagctga atgatgccac ccggaaaggac cattatccac tcccttcatt ggaccaaatg 240  
cttgcggac ttgcgggca atcttattat tgtttctgg atggatattc tggttataat 300  
cagattgatg tagatccaa ggatcaagag aagactgctt tcacctaccc tttgggtgta 360  
ttcgctatc ggcgcattgc ctgggttg tgcaatgccc cagctacatt tcagaggtgt 420  
atgatgacta tttttctga tatggtgaa aaatgaattg aagtttcat ggacgatttc 480  
tctattttg ggccatctt tgaagggtgc ttatcaaatc ttgaaagagt attaaagaga 540  
cgtgaagagt ccaaactagt tctcaattgg gagaatgcc atttcatggt tcaagaagga 600

atagtgtggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660  
taatagagaa actacctcct cccatgaat tcaaggaaat aagaagcttc cttagacatg 720  
cagggttcta caagcgattc atcaaagatt tcacaaaggt t 761

<210> 151  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 151  
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr  
35 40 45

Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn  
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr  
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile  
130 135 140

Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg  
165 170 175

Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser

195

200

205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 152  
<211> 762  
<212> DNA  
<213> Glycine max

<400> 152  
gtgcggaaag aggtattcaa gttactagag gcagggctca tctacccaat ttcatatgc 60  
tcctgggtta gtccgggtca agttgttcca aaaaaaggag ggatgacagt ggtaaaaat 120  
gatagaaaatg agctaattcc tacaagaaga gtcaccagat ggagaatgtg tattgattat 180  
aggaagctca atgaagccac aagaaaagac cattacccac ttcccttcat ggtcaaatg 240  
cttaagagac ttgcaaggca atccttctac cgtttcttgg acggataactc agttacaat 300  
cagattgcag tggatcctca ggtcaagaa aaaacagctt ttacatgtcc ttcatgttt 360  
tttgcttatac gccgcattgc gttcggtta tgtaatgcct ctactactt tcagagatgt 420  
atgatggcaa ttttgatga catggtagag aaatgtattt aagtctttat ggtgatgtt 480  
tcgttcttg gtgcatttt tggaaattgc ttagcaaatt tagagaaagt gttacaacgt 540  
tgtaaaaat ctaatttggt gcttaactgg gaaaaatgtc actttatggt acaagaaggt 600  
attgtgctag gacacaaaat ctctaaaaga ggaattgagg tggtaaaga aaaactagat 660  
gttattgata aacttccacc cccagttat gtaaaaggca tacacagttt ttgggtcat 720  
gttggatttt atcggcgatt cataaaggac ttcaccaaaag tt 762

<210> 153  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 153

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Ser Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Lys Asn Asp Arg Asn Glu Leu Ile Pro Thr  
35 40 45

Arg	Arg	Val	Thr	Arg	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
50							55						60		
Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met															
65							70					75			80
Leu Lys Arg Leu Ala Arg Gln Ser Phe Tyr Arg Phe Leu Asp Gly Tyr															
							85					90			95
Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr															
							100					105			110
Ala Phe Thr Cys Pro Phe Ser Val Phe Ala Tyr Arg Arg Met Pro Phe															
							115					120			125
Gly Leu Cys Asn Ala Ser Thr Thr Phe Gln Arg Cys Met Met Ala Ile															
							130					135			140
Phe Asp Asp Met Val Glu Lys Cys Ile Glu Val Phe Met Asp Asp Phe															
							145					150			160
Ser Phe Phe Gly Ala Ser Phe Gly Asn Cys Leu Ala Asn Leu Glu Lys															
							165					170			175
Val Leu Gln Arg Cys Glu Lys Ser Asn Leu Val Leu Asn Trp Glu Lys															
							180					185			190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser															
							195					200			205
Lys Arg Gly Ile Glu Val Val Lys Glu Lys Leu Asp Val Ile Asp Lys															
							210					215			220
Leu Pro Pro Pro Val Asn Val Lys Gly Ile His Ser Phe Leu Gly His															
							225					230			240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val															
							245					250			

<210> 154  
<211> 761  
<212> DNA  
<213> Glycine max

<400> 154  
gtgcgttaaag aagtttgaa gctgctagaa gcagacacctta tttatcccat ttcggatagt 60  
acatgggtta gccttgttca agtttgtcccc gagaaaaggag gtatgacagt cattaaagaat 120

gataaagatg agttgatatac cacaaggact gtcaccgggt gagaatgtgc attgactatc 180  
ggaagctgaa tcatgccacc cagaaggacc attattcaact cccttcatg gaccagatgc 240  
ttgaaagact tgccggacaa tcctattatt gtttctgaa tggatactct ggctataatc 300  
agattgttgt agatccaaa gatcaggaga aaactgctt cacctgcctt tttggtgtat 360  
ttgcatacaa gcgtatgcat ttggcttgt gtaatgctcc aactacgtgt cagaggtgta 420  
tgatgactat ttttctggt atcgtggaaa aatgcattga actttcatg gacgatttct 480  
ctatTTTgg gccatctttt gaaggctact tatcaaacct tgaaagagta ttacagagat 540  
gtgaagagtc taatctagtt ctcaattggg agaaatgcc a tttcatgggtt caagaaggaa 600  
tagtgctggg gcataaaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660  
taattgagaa actacctcct cccatgattt tcaaggaaat aagaagcctc ctaggacatg 720  
tagggttcta caggcgattc atcaaagact tcacaaaggt t 761

<210> 155

<211> 254

<212> PRT

<213> Glycine max

<400> 155

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Asp Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Thr Trp Val Ser Pro Val Gln Val Val Pro Glu Lys  
20 25 30

Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr  
35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Asp Ala Thr Gln Lys Asp His Tyr Ser Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asn Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr  
100 105 110

Ala Phe Thr Cys Leu Phe Gly Val Phe Ala Tyr Lys Arg Met His Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Thr Thr Cys Gln Arg Cys Met Met Thr Ile  
130 135 140

Phe Ser Gly Ile Val Glu Lys Cys Ile Glu Leu Phe Met Asp Asp Phe  
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Tyr Leu Ser Asn Leu Glu Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Met Ile Val Lys Gly Ile Arg Ser Leu Leu Gly His  
225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 156

<211> 762

<212> DNA

<213> Glycine max

<400> 156

gtgcgttaagg aggttttaa gttgctggaa gcaggtctta tttatcccat ttccggatagt 60  
gcatgggtta gccctgtgca gggtgtcccc aagaaaagaag gtaagacagt cattaaggat 120  
aaaaaaagatg agttgatatac cacaaggact atcacccgggt ggagaatgtg cattgactat 180  
cagaagctga atgatgccac ccggaaaggac cattatccac tcccttcat ggaccaaatg 240  
cttggaaagac ttgcgggca atcttattat tgtttctgg atggatattc tggttataat 300  
cagattgatg tagatcccaa ggtatcaagag aagactgctt tcacctaccc ttttggtgta 360  
ttcgcctatc ggcgcattgcc ctgggtttg tgcaatgccc cagctacatt tcagaggtgt 420  
atgatgacta tttttctga tatggtgaa aaatgaattt aagtttcat ggacgatgtc 480  
tctatttttgg ggcattttt tgaagggtgc ttatcaaattc ttgaaagagt attaaagaga 540  
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatttgt tcaagaagga 600  
atagtgttgg ggcataaaat ttcaagtaaga gggatagagg tggacaaggc aaagattgtat 660  
gtaatagaga aactacctcc tcccatgaat gtcaaggaa taagaagctt cctaggacat 720  
gcagggttct acaagcgatt catcaaagac ttctcaaaag tt 762

<210> 157

<211> 254

<212> PRT

<213> Glycine max

<400> 157

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro

1

5

10

15

Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr  
35 40 45

Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn  
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr  
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile  
130 135 140

Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Val  
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg  
165 170 175

Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Ser Lys Val  
245 250

<210> 158  
<211> 761  
<212> DNA  
<213> Glycine max

<400> 158  
gtgcggaagg aggttcttaa gctcctggaa gcagggctca tctatcttat ctcagatagt 60  
gttgggtgag tccagtgcattt gttgggtccca agaagggtgg gaagactgtg gtgagaaatg 120  
agaaaaaatga cctcattcta acccgaactg tcacaggatg gagaatgtgc atagattatc 180  
ggaagttgaa tgatgccatc aagaaggatc acttccctt accattcata gatcagatgc 240  
ttgagaggtt agcaagccag tctttcttattt atttcttggaa tgaatattctt agataacaatc 300  
agattgctat acatccaaag gaccaagaga agattgcatt tacatgccca tttgggtgtct 360  
ttgcctatag aaggatgcca tttgaactat gcaatgctcc agtaccctt tagaggcata 420  
tgctagccat attcgctaac atggtggaga aatgcatacgatg tgaatattttt 480  
cggtgtttgg tccatccctt gtttgggtt tgaccaattt agagctagtg ttgaagtact 540  
gtgaggagac aaatttagta ttgaattggg agaaatgtca tttcatggtc caagaaggaa 600  
ttatgttggg gcataaaaattt tttgctagag gtattgaggt ggacaaggcc aaaattgatg 660  
ttattgaaaa gctgcctcca ccagtcaatg taaaaggcat caggagttt cttggacaca 720  
ctgggttctt caggcgtttc atcaaggact tcacaaaatgt t 761

<210> 159  
<211> 254  
<212> PRT  
<213> Glycine max

<400> 159  
Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu  
1 5 10 15  
  
Ile Ser Asp Ser Ala Trp Val Ser Pro Val His Val Val Pro Lys Lys  
20 25 30  
  
Gly Gly Lys Thr Val Val Arg Asn Glu Lys Asn Asp Leu Ile Leu Thr  
35 40 45  
  
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60  
  
Asp Ala Ile Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80  
  
Leu Glu Arg Leu Ala Ser Gln Ser Phe Tyr Tyr Phe Leu Asp Glu Tyr  
85 90 95  
  
Ser Arg Tyr Asn Gln Ile Ala Ile His Pro Lys Asp Gln Glu Lys Ile  
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125  
  
 Glu Leu Cys Asn Ala Pro Ala Thr Phe Glx Arg His Met Leu Ala Ile  
 130 135 140  
  
 Phe Ala Asn Met Val Glu Lys Cys Ile Glu Val Phe Ile Asp Asp Phe  
 145 150 155 160  
  
 Ser Val Phe Gly Pro Ser Phe Val Cys Cys Leu Thr Asn Leu Glu Leu  
 165 170 175  
  
 Val Leu Lys Tyr Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
  
 Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Phe  
 195 200 205  
  
 Ala Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220  
  
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
  
 Thr Gly Phe Phe Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 160  
 <211> 762  
 <212> DNA  
 <213> Pisum sativum

<400> 160  
 gtgcgcagg aagtactcaa gttgttagat tcggaatga tttacccat ttctgacagc 60  
 tcgtggtaa gtccagtgc a cgtggatcca a aaaaaggag gaacctca gttttaat 120  
 gaaaagaatg aactgatccc aactcgaca gtgacagggt ggcgagttatg catcgatcac 180  
 agaagactga acacagcaac a aaaaaggat catttcctc tccctttat tgatcaaatg 240  
 ttagaaagac ttgcaggta tgagtattat tgctttctgg atggatattc gggatacaat 300  
 caaattgtt tagccccgga agatcagggaa aaaactgcatttacatgtcc ttatggattt 360  
 ttgccttaca gacggatgcc atttggctt tgcaatgccc cagctacttt tcagagggtt 420  
 atgacatcta tattctccga catgcttggaa aagtatatga aggtgtttat ggatgatttc 480  
 tctgtgttg gttcttcttt tgataattgt ttagcttaact tgtctttgt tttgcaaaga 540  
 tgcaggaaa ctaacctgt tctcaattgg gagaatgtc atttcatggt gcagggaa 600  
 attgtgctag gacacaaaat ttcccacaaa ggaattgaag tggacaaagc caaagtggag 660  
 gttatagcta acctccacc tccggtaat gaaaaaggga taaggagttt tttgggtcat 720  
 gcaggaaaa atcgcaggat catcaaagac ttcacaaagg tt 762

<210> 161  
<211> 254  
<212> PRT  
<213> Pisum sativum

<400> 161  
Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro  
1 5 10 15  
  
Ile Ser Asp Ser Ser Trp Val Ser Pro Val His Val Val Pro Lys Lys  
20 25 30  
  
Gly Gly Thr Ser Val Ile Leu Asn Glu Lys Asn Glu Leu Ile Pro Thr  
35 40 45  
  
Arg Thr Val Thr Gly Trp Arg Val Cys Ile Asp His Arg Arg Leu Asn  
50 55 60  
  
Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80  
  
Leu Glu Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95  
  
Ser Gly Tyr Asn Gln Ile Val Val Ala Pro Glu Asp Gln Glu Lys Thr  
100 105 110  
  
Ala Phe Thr Cys Pro Tyr Gly Ile Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125  
  
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Thr Ser Ile  
130 135 140  
  
Phe Ser Asp Met Leu Glu Lys Tyr Met Lys Val Phe Met Asp Asp Phe  
145 150 155 160  
  
Ser Val Phe Gly Ser Ser Phe Asp Asn Cys Leu Ala Asn Leu Ser Leu  
165 170 175  
  
Val Leu Gln Arg Cys Gln Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190  
  
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205  
  
His Lys Gly Ile Glu Val Asp Lys Ala Lys Val Glu Val Ile Ala Asn  
210 215 220

Leu Pro Pro Pro Val Asn Glu Lys Gly Ile Arg Ser Phe Leu Gly His  
225                    230                    235                    240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245                    250

<210> 162  
<211> 762  
<212> DNA  
<213> Pisum sativum

<400> 162  
gtgcgttaagg aggtctttaa actattggat gcgggaatga tttacccgat ctcggatagt 60  
ccgtgggtta gtcccggtca cgtgggtccg aagaagggtg gaatgaccgt aatccgtaat 120  
gacaaagacg aattgatccc gactaaagtt gcaacggggt ggagaatatg tataagattat 180  
agacagttga ataccgcac tcgaaaggac cattttccac tcccatttat ggatcaaatg 240  
cttggaaagac tatcgggcca acaatactat tgtttcttgg acggctactc cggttacaac 300  
caaattgcgg ttgaccgggt tgatcatgag aagacggctt tcacgtgtcc gtttggagtg 360  
ttcgcataca gaaaaatgcc ctggggctg tgcaatgcac cggcgacttt ccaacgatgc 420  
gtccttagcca ttttgccga tctaatacgag aaaacaatgg acgtcttcat ggatgacttc 480  
tcggtatttg gtggacggt tagtctatgc ttggcaaatt tgaagacggt gttggaaagg 540  
tgtgtgaaga ccaatttggc gctaaatgg gaaaagtgtc acttcatggt gaccgagggg 600  
atcgtcttag gccacaaagt ctctaaaagg gggcttgaag tggatagagc taaggttgaa 660  
gtaattgaaa aattaccccc tccgggtgaat gtgaaaggca tccgttagctt tttggggcac 720  
gcggggttt accggcgctt cattaaagac ttctcaaaag tt                    762

<210> 163  
<211> 254  
<212> PRT  
<213> Pisum sativum

<400> 163  
Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro  
1                    5                    10                    15

Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys  
20                    25                    30

Gly Gly Met Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr  
35                    40                    45

Lys Val Ala Thr Gly Trp Arg Ile Cys Ile Asp Tyr Arg Gln Leu Asn  
50                    55                    60

Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met

65

70

75

80

Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Val Asp His Glu Lys Thr  
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile  
130 135 140

Phe Ala Asp Leu Ile Glu Lys Thr Met Asp Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Phe Gly Gly Thr Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr  
165 170 175

Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
245 250

<210> 164

<211> 762

<212> DNA

<213> Pisum sativum

<400> 164

gtgcggaagg aggtctttaa attgttgat gcggggatga tttacccat ctcggatagt 60  
ccatgggtta gtcctgtca cggtgtccg aagaaggggg ggattaccgt aatccggaat 120  
gacaaggatg aattgatccc cactaaagtt gaaacgggtt ggagaatgtg tattgattat 180  
aggcggttga ataccgcgac tcgaaaagac cattttccac tccccattat ggatcaaatg 240  
ctcggaaagac tatcgggcca acaatattat tggttttgg acggctactc cggttacaac 300  
caaattgcgg ttgacccggc cgatcatgag aagacggctt tcacatgtcc gttggagtg 360

ttcgcatacc gaaaaatgcc ctttgggctg tgcaatgcac cgccgacctt ccaacgatgt 420  
gtccaagcca ttttgtcga tctgatagag aaaacaatgg aagtcttcat ggatgacttc 480  
tcggtatgg gtgggtctt tagtctatgc ttggcgaact tgaaaacggg gttggagaga 540  
tgtgtgaaga ccaatttgtt gcttaattgg gagaagtgtc acttcatggt gaccgagggg 600  
atcgtagctag gccacaaagt ctctagaagg gggcttgaag tggatagagc taaggttcaa 660  
gtgatagaaa aattacctcc tccggtaat gtgaaggca tccgaagctt tttggggcac 720  
gccgggttct accggcgctt cattaaagat ttcacaaagg tt 762

<210> 165

<211> 254

<212> PRT

<213> Pisum sativum

<400> 165

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys  
20 25 30

Gly Gly Ile Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr  
35 40 45

Lys Val Glu Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Arg Leu Asn  
50 55 60

Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Ala Asp His Glu Lys Thr  
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Gln Ala Ile  
130 135 140

Phe Val Asp Leu Ile Glu Lys Thr Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Phe Gly Gly Ser Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr  
165 170 175

Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Arg Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250